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Result
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Perfect score:
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           Pred. No. is the number of results predicted by chance score greater than or equal to the score of the result and is derived by analysis of the total score distribut
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length: 2000000000
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Copyright (c) 1993 - 2000 Compugen Ltd
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/cgn2_6/ptcodata/1/paa/US06_NEW_COMB.pep:*
/cgn2_6/ptcodata/1/paa/US08_NEW_COMB.pep:*
/cgn2_6/ptcodata/1/paa/US08_NEW_COMB.pep:*
/cgn2_6/ptcodata/1/paa/US09_NEW_COMB.pep:*
/cgn2_6/ptcodata/1/paa/US10_NEW_COMB.pep:*
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         2002, 16:26:01; Search time 79.2 Seconds (without alignments) 380.853 Million cell updates/sec
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US-10-105-0572-10
US-10-105-171-10
PCT-US02-16106-641
US-10-139-785-66
US-10-139-785-66
US-09-855-544A-13
US-10-113-80-82
US-10-119-480-82
US-10-119-480-82
PCT-US02-16106-44
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US-09-579-548A-1
US-10-1151-882-40
US-10-1151-882-40
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US-10-1151-882-40
US-10-1151-882-40
US-10-136-511-3
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Sequence 2, Appli
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RESULT 2
US-09-671-658A-2
; Sequence 2, Application
; GENERAL INFORMATION:
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PCT-US02-09271-2
; Sequence 2, Application PC/TUS0209271
; GENERAL INFORMATION:
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 316
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                                                                                                                                          263
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ALIGNMENTS

Query Match 99.6%; Best Local Similarity 99.7%; 121 PAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHKVTLSSWYHDRGWAKISNWTLSN 180 WSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKVQDID 294 WSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKVQDID Conservative Score 1554; DB 1; Pred. No. 7.9e-132; "'~matches 1; Length Indels 316; 316 0; Gaps 82 60 0

US/09671658A

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RESULT 3
US-10-105-057-2
; Sequence 2, Application US/10105057
; GENERAL INFORMATION:
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Best Local :
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APPLICANT: Barnes-Jewish Hospital, d/b/a The Jewish Hospital of St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0686
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
TELEPAX: (650)496-1204
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                              143
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CLASSIFICATION: <UNKnown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/989,362
FILING DATE: 12-DEC-1997
APPLICATION NUMBER: US 60/032,846
FILING DATE: 13-DEC-1996
ATTORNEY, ACENT INFORMATION:
                                                                                                                                                          241 WSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKVQDID 294
                                                                                                                                                                                                                 203
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Mammalian Cell Surface Antigens; Related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Gorman, Daniel M
                                                                                                                                                                                                               GKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVYVVKTSIKIPSSHNLMKGGSTKN
                                                                                                                                                                                                                                   GKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMYYVVKTSIKIPSSHNLMKGGSTKN 240
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                                                                                                                                        WSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKVQDID 316
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STATE: California
COUNTRY: USA
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Pred. No. 7.9e-132;
0; Mismatches 1;
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 316
TYPE: PRT
ORGANISM: Mus musculus
US-10-105-057-2
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멍
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PCT-US02-16002-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 10, Application PC/TUS0216002 GENERAL INFORMATION:
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Best Local Similarity
Matches 293; Conserv
                                                                                                                                    Query Match
Best Local Similarity
Matches 250; Conserva
                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn version 3.1 SEQ ID NO 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Immunex Corporation APPLICANT: DOUGALL, William APPLICANT: ANDERSON, Dirk
                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: PCT/US02/16002
CURRENT FILING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: 60/291,919
PRIOR FILING DATE: 2001-05-17
                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: THERAPEUTIC FILE REFERENCE: 3277-WO
                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 10
                                                                                                                                                                                                                                                        LENGTH: 317
TYPE: PRT
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 82
                              61 DSTHCFYRILRLHENADLQDSTLESEDT--LPDSCRRMKQAFQGAVQKELQHIVGPQRFS 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKVQDID 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVYVVKTSIKIPSSHNLMKGGSTKN 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHKVTLSSWYHDRGWAKISNMTLSN 180
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                                                                  GAPHEGPLH-APPPPAPHQPPAASRSMFVALLGLGLGQVVCSVALFFYFRAQMDPNRISE
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Conservative
                                                                                                                                       Conservative
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                                                                                                                                       85.0%; Score 1326.5; DB 1;
84.5%; Pred. No. 2.2e-111;
tive 16; Mismatches 27;
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Pred. No. 7.9e-132;
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PCT-US02-16106-41
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US-10-151-071-10
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                          Sequence 41, Application PC/TUS0216106
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Antibodies Against Tumor Necrosis
FILE REFERENCE: PF554PCT
CURRENT APPLICATION NUMBER: PCT/US02/16106
CURRENT FILING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: 60/293,100
PRIOR FILING DATE: 2001-05-24
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Best Local Similarity
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SEQ ID NO 10
LENGTH: 317
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PRIOR FILING DATE: 2001-05-17
NUMBER OF SEQ ID NOS: 10
SOFTWARE: 000: 10
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TITLE OF INVENTION: THERAPEUTIC USES OF RANK ANTAGONISTS
FILE REFERENCE: 3277-A
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CURRENT APPLICATION NUMBER: US/10/151,071
CURRENT FILING DATE: 2001-05-17
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               NUMBER OF SEQ ID NOS: 48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DSTHCFYRILRLHENADLQDSTLESEDT--LPDSCRRMKQAFQGAVQKELQHIVGPQRFS 118
                                                                                                                                                                                                                                                                                                                                   SNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVYVVKTSIKIPSSHNLMKGGST 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     DGTHCTYRILRLHENADFQDTTLESQDTKLTPDSCRRIKQAFQGAVQKELQHTVGSQHTR 141
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PatentIn version 3.0
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Pred. No. 2.2e
16; Mismatches
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es 27;
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; ORGANISM: Homo sapiens US-10-039-785-66
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US-10-039-785-66
; Sequence 66, A
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; ORGANISM: HOMO
PCT-USO2-16106-41
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PRIOR FILING DATE: 2002-04-05
PRIOR PRIOR PELICATION NUMBER: 60/341,237
PRIOR PELICATION NUMBER: 60/331,310
PRIOR APPLICATION NUMBER: 60/331,310
PRIOR APPLICATION NUMBER: 60/331,310
PRIOR APPLICATION NUMBER: 60/331,044
PRIOR FILING DATE: 2001-11-07
PRIOR PELICATION NUMBER: 60/327,364
PRIOR PELICATION NUMBER: 60/323,807
PRIOR APPLICATION NUMBER: 60/323,807
  Query Match
Best Local Similarity
Matches 78; Conserv
                                                                                                                                                                                      SEQ ID NO 66
LENGTH: 281
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LENGTH: 281
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                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 60/
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                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 66
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                                                                                                                                                                                                                                                                                PRIOR FILING DATE:
                                                                                                                                                                   TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVYVVKTSIKIPSSHNLMK 234
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78; Conserv
                                                                                                                                                                                                                                    PatentIn
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16.6%; Score 258.5; DB 6; 26.4%; Pred. No. 1.9e-15; tive 54; Mismatches 113;
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Pred. No. 1.9e-15;
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FILE REFERENCE: PF554
CURRENT APPLICATION NUMBER: US/10/151,882
CURRENT FILING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: 60/293,100
PRIOR FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 48
SOFTWARE: Patentin version 3.0
SEQ ID NO 41
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US-10-151-882-41
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US-10-139-785-66
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Best Local S
Matches 78
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Sequence 66, Application US/10139785
GENERAL INFORMATION:
APPLICANT: Salcedo et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
TITLE OF INVENTION: Receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
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TYPE: PRT
ORGANISM: Homo sapiens
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Local Similarity 26.4%;
hes 78; Conservative 54
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                                                                                                                                                                                                                  GGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKV 290
                                                                                                                                                                                                                                                               NLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYT-SYPDPILLMK
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                                                                                                                                                                                                                                                                                                                                                                            EGSWLDVAQRGKPEAQPFAHLT----INAASIPSGSHKVTL----SSWYHDR-GWAKIS 174
                                                                                                                                                                                                                                                                                                                                                                                                                        WDP--NDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPL-----
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                                                                                                                                                                                 SARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV
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Pred. No. 1.9e-
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9e-15;
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CURRENT FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: 60/369,860
PRIOR APPLICATION NUMBER: 60/369,860
PRIOR TILING DATE: 2002-04-05
PRIOR PRILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: 60/341,237
PRIOR APPLICATION NUMBER: 60/331,310
PRIOR APPLICATION NUMBER: 60/331,310
PRIOR FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/331,044
PRIOR APPLICATION NUMBER: 60/331,044
PRIOR APPLICATION NUMBER: 60/337,364
PRIOR APPLICATION NUMBER: 60/327,364
PRIOR APPLICATION NUMBER: 60/327,364
PRIOR APPLICATION NUMBER: 60/327,364
PRIOR FILING DATE: 2001-10-09
PRIOR FILING DATE: 2001-10-99
PRIOR FILING DATE: 2001-09-21
PRIOR FILING DATE: 2001-09-21
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; ORGANISM: Homo sapiens
US-09-855-544A-13
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GENERAL INFORMATION:
APPLICANT: RODITION: SEQUENCES OF TRAIL VARIANTS
TITLE OF INVENTION: SEQUENCES OF TRAIL VARIANTS
FILE REFERENCE: 2786-0173P
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                                         SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 13
LENGTH: 246
TYPE: PRT
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                                                                                                                            CURRENT APPLICATION NUMBER: US/09/855,544A
CURRENT FILING DATE: 2001-05-19
NUMBER OF SEQ ID NOS: 16
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RESULT 12
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TITLE OF INVENTION: DNA Cassette for the Production of
TITLE OF INVENTION: Secretable Recombinant Trimeric Trail Proteins, Tetracycline
TITLE OF INVENTION: Combination and Use in Gene-Associated Virus Vector, Their
TITLE OF INVENTION: Combination and Use in Gene Therapy
FILE REFERENCE: 5006-1-002
CURRENT FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: KR 2000-38441
PRIOR APPLICATION NUMBER: KR 2000-07-06
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
LENGTH: 168
Sequence 29, Application US/10116378
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin
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Best Local :
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Best Local
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ORGANISM: homo sapiens
                                                                                                                                                                                                 118 WSKDAEYGLYSIYQGGTFELKENDRIFYSVTNEHLIDMDHEASFFGAFLV 167
                                                                                                                                                                                                                                                                                                                 181 GKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVYVVKTSIKIPSSHNLMKGGSTKN 240
                                                                                                                                                                                                                                                                                                                                                                                                   131 VAQRGKPEAQPFAHLT-----INAASIPSGSHKVTL----SSWYHDR-GWAKISNMTLSN 180
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                                                                                                                                                                                                                                                                                                                                                                        | VRERGPORVA--AHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRN 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 14.9%; Score 232; DB 5; Length 246; Local Similarity 25.0%; Pred. No. 3.9e-13;
                                                                                                                                                                                                                                                                                      GELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYT-SYPDPILLMKSARNSC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SQTYFRFQEEIKENTKNDKQMVQYIYKYT-SYPDPILLMKSARNSCWSKDAEYGLYSIYQ 209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 168;
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Matches 36; Conservative
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; ORGANISM: Homo Sapien US-10-119-480-82
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                                                                                                                                                             SEQ ID NO 82
LENGTH: 95
TYPE: PRT
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CURRENT FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/247,225
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/247,225
PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-09
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/074,087
PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-09
NUMBER OF SEQ ID NOS: 31
SEQ ID NO 29
LENGTH: 164
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                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/119,480 CURRENT FILING DATE: 2002-04-09 NUMBER OF SEQ ID NOS: 246
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Grimaldi, J. Ch
APPLICANT: Gurney, Austin
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APPLICANT:
                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3530P1C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Baker, Kevin APPLICANT: Desnoyers, I
                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Stephan, Jean-Philippe F. APPLICANT: Watanabe, Colin L. APPLICANT: Wood, William I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: NOVEL TUMOR NECROSIS FACTOR RECEPTOR HOMOLOG AND TITLE OF INVENTION: NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P1206R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     113 GPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLT----INAASIPSGSHKVTL----SS 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                156 SFFGAFLV 163
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Grimaldi, J. Christopher
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Smith, Victoria
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Pitti, Robert M.
Wood, William
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                       11.3%;
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Score 176; DB 6;
Pred. No. 1.2e-08;
6; Mismatches 21
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                                             Length 95;
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PCT-US02-16106-44
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PCT-US02-16106-44
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Best Local S
Matches 67
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SEQ ID NO 44
LENGTH: 281
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                                                                                                                                          APPLICANT: Yu et al.
                                                                                                                                                                       Sequence 6, Application US/09588947A
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CURRENT FILING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: 60/293,100
PRIOR FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 48
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                                CURRENT FILING DATE: 2000-06-08
PRIOR APPLICATION NUMBER: 09/588,947
PRIOR FILING DATE: 2000-06-08
                                                                     TITLE OF INVENTION: Diagnostic Methods Using FILE REFERENCE: PF343P3C2 CURRENT APPLICATION NUMBER: US/09/588,947A CURRENT FILING DATE: 2000-06-08
PRIOR APPLICATION NUMBER: 09/507,968 PRIOR FILING DATE: 2000-02-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLT--INAASIPSGSHKVTLS 162
                                                                                                                                                                                                                                                                                                                                    NSKYPQDLVMME-GKMMSYCTTGQMWARSSYLGAVFNLTSADHLYVNVSELSLVNFEESQ 273
                                                                                                                                                                                                                                                                                                  TYFGAFKV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43;
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SEQ ID NO 6
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                 223
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                                                                                                                                                                                                                                                                                                                                      Local Similarity
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FILING DATE: 1999-07-06
APPLICATION NUMBER: 60/145,824
FILING DATE: 1999-07-27
APPLICATION NUMBER: 60/167,239
FILING DATE: 1999-11-24
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FILING DATE: 1999-04-16
APPLICATION NUMBER: 60/130,696
FILING DATE: 1999-04-23
APPLICATION NUMBER: 60/131,278
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APPLICATION NUMBER: 60/124,097
FILING DATE: 1999-03-12
APPLICATION NUMBER: 60/126,599
FILING DATE: 1999-03-26
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APPLICATION NUMBER: 60/131,673
FILING DATE: 1999-04-29
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Dougall,W.C. and Galibert,L.
Breceptor activator of NF::kappa.B
Patent: US 6271349-A 10 07-AUG-2001;
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TACACAACGGTTTTACAATTTTGTAATGATTTCCTAGAATTGAACCAGATTGGGAGAGGT
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(RANKL) mRNA, o
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                                                                                                                                               A homologue of the TNF receptor and growth and dendritic-cell function Nature 390 (6656), 175-179 (1997)
                                                                      Direct Submission
Submitted (13-AUG-1997) Molecular Biology,
University St., Seattle, WA 98101, USA
                                                                                                       Cosman, D., DuBose, R.
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Roux,E.R., Teepe,M.C., DuBose,R.F.,
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Rodentia;
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Sciurognathi; Muridae;
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/note="receptor a
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ICFRHHETSGSVPTDYLQLMYYVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINV
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AF053713.1 G
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; I (bases 1 to 2299)
Lacey,D.L. Timms,E., Tan,H.-L., Kelley,M.J., Dunstan,C.R., Burgess,T., Elliott,R., Colombero,A., Elliott,G., Scully,S., Burgess,T., Elliott,R., Colombero,A., Elliott,G., Scully,S., Hsu,H., Sullivan,J., Hawkins,N., Davy,E., Capparelli,C., Eli,Qian,Y.-x., Kaufman,S., Sarosi,I., Shalhoub,V., Senaldi,G., Golaney,J. and Boyle,W.J. Sarosi,I., Shalhoub,V., Senaldi,G., Gosteoprotegerin ligand is a cytokine that regulates osteoclas differentiation and activation cell 93 (2), 165-176 (1998)
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Submission

ted (16-MAR-1998) Department of Cell Biology, Amgen,
gen Center Drive, Thousand Oaks, California 91320, U.

Location/Qualifiers
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/product="osteoprotegerin ligand"
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Gorman, D.M. and Mattson, J.D.
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AGAGTCTTCAG 1819
                               GGCAGAATACTGTTTCTGGTGACCACATGTAGTTTATTTCTTTATTCTTTTAACTTAAT
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RESULT 9
AF013170
LOCUS
DEFINITION
ACCESSION

AF013170 Mus musculus AF013170

TNF-related

2237 bp ligand

mRNA 1:

complete

ROD 05-NOV-1998

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VERSION
KEYWORDS
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                          1624;
 CACCCCCCCCCCCCCCCATGTTCCTGGCCCCTCCTGGGGCTGGGACTGGGCCAGGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANCE (tumor necrosis factor [TNF]-related activation-induced cytokine), a new TNF family member predominantly expressed in cells, is a dendritic cell-specific survival factor J. Exp. Med. 186 (12), 2075-2080 (1997) 98060869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and Choi,Y.

TRANCE is a novel ligand of the tumor necrosis factor receptor family that activates c-Jun N-terminal kinase in T cells
J. Biol. Chem. 272 (40), 25190-25194 (1997)
97460112
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1 (bases 1 to 2237)
Wong, B.R., Rho, J., Arron, J.,
Kalachikov, S., Cayani, E., Bal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fuller, K., Wong, B., Fox, S., Choi, Y. and Chambers, T.J.
TRANCE is necessary and sufficient for osteoblast mediated activation of bone resorption in osteoclasts
J. Exp. Med. 188 (5), 997-1001 (1998)
98401035
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J. Biol. Chem. 273 (43),
98447691
5 (bases 1 to 2237)
                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (09-JUL-1997) Howard Hughes Medical Institue, Rockefeller University, 1230 York Ave., New York, NY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wond, B.R., Rho, J., Arron, J., Lee, S.Y., Robinson, E. and Direct Submission
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                                                                                 Conservative
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ICFRHETSGSYPTDLIQLMYVYKTSIKIPSSHILMKGGSTKNWSGNSEFHFYSINV
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4 70 c 519 g 612 t
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                 /codon_start=1
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99.6%;
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Bartlett, F.S. III, Frankel, W
                                                                                    Mismatches
                                                                                                No. 0;
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AUTHORS
TITLE
JOURNAL
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DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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            Query Match 70. Best Local Similarity 99. Matches 1164; Conservative
                                                                                                        source
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                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Nammalla; Eutheria; Rodentia; Sciurognati; I (bases 1 to 2029)

Mizuno, A., Kodaira, K. and Kodaira, Y.

DNA and process for producing protein by
Patent: JP 2000102390-A 4 11-APR-2000;
SNOW BRAND MILK PROD CO LTD, YS NEW TECHNO
OS Mus sp. (mouse)
PN JP 2000102390-A/4
PD 11-APR-2000
PF 30-SEP-1998 JP 1998292971
PR ATSUKO MIZUNO, KUNHIKO KODAIRA, YASUF C12R1:91), C12R1:91)
C12R1:91,
PC (C12P21/02,C12R1:91),C12N15/00,(C12N15/09,A61K31/00,C07K14/47,C12P21/02,C12R1:91)
PC (C12P21/02,C12R1:91),C12N15/00,(C12N15/09,A61K31/00,C07K14/47,C12P21/02,C12R1:91)
PR Key Location/Qualifiers
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DNA and process for process 434349

E34349.1 GI:18624334

JP 2000102390-A/4.

Mus sp.

Mus sp.

Eukaryota; Metazos; Chc
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12N15/09,A61K31/00,C07K14/47,C12P21/02,C12Q1/68//(C12N15/09,
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/organism="Mus sp."
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a 334 c 412 g 6
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Location/Qualifiers
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GCCAACATTTGCTTTCGGCATCATGAAACATCGGGAAGCGTACCTACAGACTATCTTCAG
                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (05-JAN-1999) Kunihiko Kodaira, Chugai Pharmaceutical
Co., LTD.; 301 Fuji, 6-19 Nakamachi, Hannou-city, Saitama 357-0
Japan (E-mail:koda@takauji.or.jp, Tel:81-33987-0594)
Location/Qualifiers
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AB022038.1:146. .182,AB022038.1:274. .372,159.
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Direct Submission
Submitted (16-MAR-
One Amgen Center D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lacey, D.L., Timms, E., Tan, H.-L., Kelley, M.J., Dunstan, C.R., Burgess, T., Elliott, R., Colombero, A., Elliott, G., Scully, S., Hsu, H., Sullivan, J., Hawkins, N., Davy, E., Capparelli, C., Eli, A., Qian, Y.-X., Kaufman, S., Sarosi, I., Shalhoub, V., Senaldi, G., Guo, Delaney, J. and Boyle, W.J.

Osteoprotegerin ligand is a cytokine that regulates osteoclast differentiation and activation

Cell 93 (2), 165-176 (1998)
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AF053712
AF053712.1 G
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Amgen Center Drive, Thousand Oaks, California 91320, US
                                                                                                                                                                                                                                                                                                                                                      Conservative
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/product="acc39731.1"
/protein_id="Acc39731.1"
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SRSMFVALLGLGLGQVVCSVALFFYFRAQMDPNRISEDGTHCIYRILKLHENADFQDT
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EAOPFAHLTINATDIPSGSHKVSLSSWYHDRGAKISNMTFSNGKLIVNQDGFYYLYA
NICFRHHETSGDLATEYLQLMYVYTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSIN
VGGFFKLRSGEEISIEVSNPSLLDPDQDATYFGAFKVRDID"

VGGFFKLRSGEEISIEVSNPSLLDPDQDATYFGAFKVRDID"
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/db_xref="taxon:9606"
185. .1138
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Pred. No. 6.5e-212;
0; Mismatches 314;
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                         ATGCTGGAACCTGCAAAAAATAC---TTTTTCTAATGAGGAGAG-AAAATATATGTATTT
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REFERENCE
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AF019047
                                                                                                      BASE COUNT
ORIGIN
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
                                             Query Match
Best Local
                               Matches 1285;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 (bases 1 to 2201)
Anderson, D.M., Billingsley, W., Dougall, W.,
Cosman, D., DuBose, R. and Galibert, L.
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Nature 390
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                                 Conservative
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                                                                                                                                                                /protein_id="AAB86811.1"
/protein_id="AAB86811.1"
/db_xref="G1:2612922"
/db_xref="G1:2612922"
/translation="MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPPAPHQPPAA
SRSMFVALLGLGGVCSVALFTYFRAQMDPNRISEDGTHCTYRILELHENADFQDT
TLESQDTKLIPDSCRRIKQAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKL
EAQPFAHLTINATDIPSGSHKVSLSSWYHDRGWAKISMMTFSNGKLIVNQDGFYYLYA
EAQPFAHLTINATDIPSGSHKVSLSSWYHDRGWAKISMTFSNGKLIVNQDGFYYLYA
                                                                                                                     NICFRHHETSGDLATEYLOLMYYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSIN
VGGFFKLRSGEELSIEWSNPSLLDPDQDATYFGAFKVRDID"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                          /product="RANKL"
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                                                                                                                                                                                                                                                                                                       note="receptor"
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                                             57.0%;
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                               Score 928.6; DB 9;
Pred. No. 2.6e-209;
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Teepe,M.C., DuBose,R.F.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
AUTHORS
Mizuno,A., Kodaira; K. and Kodaira,Y.
DNA and process for producing protein by using the same
Patent: JP 2000102390-A 5 11-APR-2000;
SNOW BRAND MILK PROD CO LTD,YS NEW TECHNOLOGY LAB
OS MUS SP. (mouse)
PN JP 2000102390-A/5
PD 11-APR-2000
PF 30-SEP-1998 JP 1998292971
PR
ATSUKO MIZUNO,KUNIHIKO KODAIRA,YASUKO KODAIRA PC
C12N15/09,A61K31/00,C07K14/47,C12P21/02,C12Q1/68//(C12N15/09, PC
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DNA and process for producing

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Mammalia; Eutheria; Rodentia; Sciurognathi.
1 (bases 1 to 951)
Kyoji, Y.N.S.S. and Tsuda, T.M.K.K.
Novel protein, DNA and utilization thereof
Patent: JP 199332581-A 1 07-DEC-1999;
SNOW BRAND MILK PROD CO LTD, SANKYO CO LTD
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KANJI HIGASHIO
C12N15/09, A61K31/00, A61K38/00, A61K45/00, C07K14/47, C07K16/18,
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Search completed: July 8, 2002, 23:50:08 Job time: 13447 sec

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Result
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activator; human; shock; sepsis; F; mouse; ss.	; NF-kB; receptor response; toxic s crosis factor; TNF	kappa I mmatory mour ne	or- fla	is fa nse; ligan	0 =	RANK; immun RANKL
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CMV-derived leader	AAD18399	22	768	ω.	58.4	43
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Mouse OBM nucleoti	AAA39154	212	575	ກ ເກ ກ	105.8 58.4	40
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Mouse OBM nucleoti	AAA39152	21	2026	9.7	157.8	38
encoding	AAZ99970 AAA39153	2 21	564 468	10.2	165.8	3 7 7
encoding	AAZ99973	21	519	15.9	259.4	ω
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encoding	AAZ99969	2 2	519	19.2	278 6	ω ω Δ Κ
	AAZ99968	21	519	19.2	312.2	31
Mouse cDNA encodin	AAZ99967	21	564	19.2	313.2	30
Nucleic acid encod	AAV69899	19	741	31.9	520.6	ა გა დ დ
Nucleic acid encod	AAV69887	19	954	37.5	611.8	27
Human receptor act	AAD08715	3 2	954	37.7	615	2 2
Human receptor act	AAD15311	22	954	37.7	615	24
NF-kB receptor act	AAV41378	4 L	954	37.7	615	23
Nucleic acid encod	AAV69898	19	735	45.0	733.4	22,22
Nucleotide sequenc	AAH25526	22	1574	46.9	764.6	20
Human TRANCE encod	AAF86481	٥ د د	957	47.4	773.4	19
Osteoclast formati	AAZ49024	27	1831	л (л 1 — (.)	832.4	18
DNA encoding a mur	AAZ99965	21	951	54.3	885.4	16
Mouse OBM nucleoff	AAA39156	21	951	54.3	885.4	15
Nucleotide sequence	AAV69900	19	951	54	885.4	14
DNA encoding a hum	AAZ99964 AAV70085	1 2 1 4	2274	57.6	939.6	13
Mouse OBM nucleoti	AAA39155	2 22	2029	70.7	1152.4] <u> </u>
Nucleic acid encod	AAV69886	19	1538	82.7	1348.4	10

RESULT 1 AAV41377 ID AAV41377; ID AAV41377; XX AC AAV41377; XX AC AAV41377; XX DT 08-OCT-1998 (first entry) XX DE NF-kB receptor activator RANK ligand (RANKL) encoding cDNA XX KW Immune response; inflammatory response; toxic shock; sepsi KW RANKL; RANK ligand; tumour necrosis factor; TNF; mouse; ss XX OS Mus musculus. XX FH Rey Location/Qualifiers FT CDS 3..887 FT

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This cDNA encodes a murine RANKL, a ligand for the RANK (receptor cc activator of necrosis factor-kappaB (NF-kB)) polypeptide. RANK is a cc member of the tumour necrosis factor (TMP) family. A soluble RANK cc may be used for inhibiting activation of NF-kB, by contacting a cell cc expressing membrane-associated RANK with a soluble RANK which binds to cc can be cc used to induce maturation of dendritic cells and enhance their cc used to induce maturation of dendritic cells and enhance their cc allo-stimulatory capacity, thereby augmenting an immune response. The cc immune or inflammatory response. Inhibition of NF-kB by RANK antagonists cc may be useful in ameliorating negative effects of an inflammatory capacity of the reactions, or acute inflammatory cresponse that result from triggering of RANK, e.g. in treating toxic shock or sepsis, graff-versus-host reactions, or acute inflammatory caponse that result from triggering of RANK, e.g. in treating toxic cc characterised by neoplastic cells that express RANK. RANKL polypeptides cc can also be used to identify inhibitors of RANK and thus inhibitors of can inflammatory response, and also for protecting RANK-expressing cells from the negative effects of chemotherapy or the presence of high levels of TNF-alpha. The products can also be used for detection and drug cc screening.
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develop products for augmenting an immune response for
inflammatory response and for protection of cells
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CTCTGTCCTCTTGGTACCACGATCGAGGCTGGGCCAAGATCTCTAACATGACGTTAAGCA
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RESULT
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  Query Match
Best Local Similarity
Matches 1630; Conserv
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 23-DEC-1996;
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CC kappaB (RANK) proteins and their corresponding DNAs. RANK is a member CC of the tumour necrosis factor (TNF) receptor superfamily and associates CC in the regulation of immune and inflammatory response. The receptors of immune and inflammatory responses. The receptors of immune and inflammatory responses. The receptors CC are useful for regulating immune response and in screening for inhibitors CC dasays for inhibitors of signal transduction, e.g. for screening the CC assays for inhibitors of signal transduction, e.g. for screening the CC are useful in ameliorating the negative effects of an inflammatory cresponse that result from triggering of RANK with TRAF1, TRAF2, TRAF3, CC RRAF5 and particularly TRAF6. NF kappaB inhibition by RANK antagonists creations and the effects of bone resorption. RANK acts as an anticce shock or sepsis, graft-versus-host reactions, acute inflammatory corresponse that result from triggering of RANK, e.g. in treating toxic shock or sepsis, graft-versus-host reactions, acute inflammatory corrections and the effects of bone resorption. RANK acts as an anticce apoptotic signal and rescue the cells that express RANK from apoptosis. Soluble forms of the receptor are used in vivo or in vitro based corrections to farmation of a signal via RANK. RANK compositions are used in the development of both agonists or antagonists of RANK activity, as an expression of disease characterised by neoplastic cells that corrections are used as inhibitors of diseases characterised by neoplastic cells that corrections and for modulating obsecolast function and activities. They are used as inhibitors of diseases associated with excess bone resorption and as immunosuppressants or anti-inflammatory agents. The RANK DNAs are used in the presence or distribution of recombinant proteins. The RANK DNAs are useful for the expression of recombinant proteins, while the proteins are useful or the resorption of soluble RANK, or monitor RANK interactions of corrections of soluble RANK, or monitor RANK light of the res
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14-OCT-1997;
23-DEC-1996;
07-MAR-1997;
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                                                  murine RANK ligand (RANKL) protein
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                                         TCTGCAGCATCGCTCTGTTCCTGTACTTTCGAGCGCAGATGGATCCTAACAGAATATCAG 180
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CD40; TNF
                           New DNA molecules, useful for producing ligands (which are useful for regulating immune response and in screening for inhibitors of NF-chi I receptor activator of NF-chi B (RANK)
                                                                                                                                                                                                                                                  Key
                                                                                                                                                                                                                                                                                      Murine; receptor activator of NF-chi B; RANK; tumour necrosis factor; CD40; TNF receptor-associated factor; TRAF; ligand; immune response; chromosome 18q22.1; RANKL; chromosome 13q14; transmembrane protein; s
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 ggcatcatgaaacatcgggaagcgtacctacagactatcttcagctgatggtgtatgtcg
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                Mouse; receptor activator of NF-kappaB; RANK; nuclear factor-kappaB; NF-kappaB; tumour necrosis factor; TNF; type I transmembrane protein; TNF receptor-associated factor; TRAF; RANK ligand; RANKL; osteopathic; inflammatory reaction; bone resorption; gene therapy; immunomodulator; immune system dysfunction; familial associate osteolysis; FEO;
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            disease of bone; EP; cytostatic;
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The present invention relates to a novel receptor, referred to as RANK CC (receptor activator of NF (nuclear factor)-kappaB), a member of TNF CC (tumour necrosis factor) receptor superfamily. RANK is a Type I CC transmembrane protein that interacts with TNF receptor associated CC factors (TRAFS) Triggering of RANK by overexpression or co-expression CC of RANK and membrane bound RANK ligand (RANKL) results in upregulation CC of the transcription factor NF-kappaB, a ubiquitous transcription factor CC inhibition of NF-kappaB by RANK antagonists is useful in ameliorating CC negative effects of inflammatory reactions, and the effects of excess CC bone resorption. The RANK DNAS, proteins and their analogues are useful CC for the preparation of pharmaceutical compositions, for infecting target CC associated with RANK, and as targets for use in screening assays. They CC may be used in the treatment or diagnosis of immune system dysfunction. CC The present invention also encompasses gene therapy methods to correct CC gene-activating mutations, associated with e.g. familial expansile CC osteolysis (FEO) and early onset Paget's disease of bone (EP). The CC present sequence is a CDNA encoding murine RANKL (muranKL) protein.
                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 1630; Conserv
                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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16-APR-1997;
23-JUN-1997;
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         encoding OPG bin
protein. OPG bin
osteoprotegrin
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                                                                                               Nucleic acid encoding osteoprotegrin binding protein - useful for, e.g. treating bone diseases by modulating osteoclast differentiation and for diagnosis {\sf Constant}
                                                                                                                                                                                                                                                                                                                                                                                                                hypercalcaemia;
Paget's disease;
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                                                                           Claim
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      present sequence encodes human osteoprotegerin (OPG) binding protein to cells transfected with vectors containing nucleic acid molecules coding OPG binding protein are used to produce recombinant OPG binding protein is used in binding assays to determine epoprotegrin (OG) in biological samples; to screen for specific
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agents

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intracellular proteins); to raise Ab (useful in immunoassays for detection of OPG binding protein) and to identify compounds that modulate binding of OPG binding protein to osteoclast differentiation and activation receptor (ODAR). The nucleic acid molecule encoding OPG binding protein can be used to detect OPG binding protein-encoding sequences, e.g. screening for related sequences, also to produce transgenic animal models, while complementary sequences are used for antisense regulation of OPG binding protein expression. Modulators of OPG binding protein, particularly soluble forms of OPG binding protein or Ab, are used to treat or prevent bone diseases, e.g. osteoporosis, bone loss caused by arthritis or metastases, hypercalcaemia, Paget's disease, periodontal disease, osteoporosis, loosening of prostneses, optionally in combination with agents that promote bone growth.
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Sequence 2295 BP; 648 A; 487 c; 538 G; 622 Η, 0 other;

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actggtcgggcaattctgaattccacttttattccataaatgttgggggatttttcaagc
          ACTGGTCGGGCAATTCTGAATTCCACTTTTATTCCATAAATGTTGGGGGATTTTTTCAAGC
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Osteoprotegerin ligand; OPGL; osteoprotegerin; osteoclastogenesis; tumour necrosis factor receptor; type II transmembrane protein;
                                        DNA encoding
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Disclosure;
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                                                                                                                                                                                                                                                                                  osteoclast differentiation; CSF-1; osteoclast activator; immune response; osteoporosis; bone resorption; ss.
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                                                                                                                  down-regulation of osteoprotegerin ligand
c, prevent and ameliorate osteoporosis -
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                                                                                                      English.
                                                                                                                        (OPGL) activity used
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The present sequence encodes a murine osteoprotegerin ligand (OPGL).

CO Steoprotegerin is a secreted member of the tumour necrosis factor receptor family, which blocks osteoclastrogenesis in a dose dependent common the open protein is synthesised as a type II transmembrane protein. The OPGL protein is synthesised as a type II transmembrane composed protein. The murine and human OPGL polypeptides are 87% homologous. OPGL is a potent osteoclast differentiation factor when combined with CSF-1. CI is not capable of inducing osteoclast differentiation in the absence cof CSF-1. OPGL is also an activator of mature osteoclasts. The cof CSF-1. OPGL is also an activator of mature osteoclasts. The cof CSF-1. OPGL is also an activator of mature osteoclasts. The cof CC opGL activity in an animal. The method comprises using at least one OPGL oplypeptide or subsequence, and/or at least one OPGL analogue to induce an immure response in the animal. The method and OPGL polypeptide are cuseful for treating, preventing and ameliorating osteoporosis or other of diseases or conditions characterised by excessive bone resorption. Sequence 2299 BP;

641 A; 494 Ç 541 G; 623 7 0 other;

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                                                      AAGACAGCACTCACTGCTTTTATAGAATCCTGAGACTCCATGAAAACGCAGATTTGCAGG
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             ACTCGACTCTGGAGAGTGAAGACACACTACCTGACTCCTGCAGGAGGATGAAACAAGCCT
actcgactctggagagtgaagacacactacctgactcctgcaggaggatgaaacaagcct
                                          aagacagcactcactgcttttatagaatcctgagactccatgaaaacgcaggtttgcagg
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This is the nucleotide sequence encoding the mouse 499E9 protein, used in the method of the invention to treat conditions associated with abnormal physiology or development. The 499E9 protein is expressed highly on polarised Th1 T cells, binding of 499E9 to its receptor may result in either immune cell expansion or apoptosis. Antagonists of 499E9 may be used to modulate immune responses in abnormal situations, e.g. autoimmune disorders including rheumatoid arthritis, systemic lupus erythematosus, Hashimoto's autoimmune thyroiditis, as well as acute inflammatory responses in which T-cell expansion, activation or immunological T-cell memory play an important role. The antibodies can be used to raise anti-idiotypic antibodies which will be useful
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                                                             ttcagggggccgtgcagaaggaactgcaacacattgtggggccacagcgcttctcaggag
     AGCCATTTGCACÁCCTCACCATCAATGCTGCCAGCATCCCATCGGGTTCCCATAAAGTCA
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                  GTACAGATGTATTTAACTGGTGCACTTTGTAATTCCCCTGAAGGTACTCGTAGCTAAGGG
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12-AUG-1997;
21-AUG-1997;
                                                           The present sequence encodes an osteoclastogenesis inhibitory factor (OCIF)-blinding molecule (OBM). The protein promotes and supports the separation and maturation of osteoclasts in the presence of bone absorption factors such as calcitriol or parathyroid hormone (PTH). OBM is isolated from stroma cells cultured in the presence of a bone absorption factor by separation and solubilisation of membrane proteins then affinity chromatography using OCIF. It exists in a full-sequence form and a solubilised form (sOBM) which is a shorter chain. OBM may be used for screening potential inhibitors and modifiers of its biological activity, and screening for receptors to OBM which mediate its function. These substances can then be used in the treatment of disorders of bone function and calcium metabolism. The antibodies can be used for assay of the protein, for investigative and diagnostic purposes, and as
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Washida N
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15-APR-1997;
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Yamaguchi
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K, Tomoyasu A,
Yasuda H;
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acatgtgtaagactactaagagacatggcccacggtgtatgaaactcacagccctctctc
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                     The present invention describes a genomic DNA encoding a protein having an activity of supporting or promoting differentiation and maturation of osteoclasts. The genomic DNA encoding a protein has the following properties: (a) combines specifically with osteoclastogenesis inhibitory factor (OCIF) and has a high affinity; (b) shows a molecular weight (mw) of 30,000 to 40,000 by SDS-PAGE (sodium dodecyl sulfate-polyacrylamide gel electrophoresis) under a nonreductive condition and the apparent mw when crosslinked with monomer type OCIF is 90,000 to 110,000; and (c) has an activity of supporting or promoting differentiation and maturation of osteoclast in the co-culture of mouse osteoblast-like stroma cell and mouse spleen cell in the presence of a bone absorption promoting factor such as active type vitamin D3 and parathyroid hormone (PTH). The protein can be used as a drug-and a research reagent. The present sequence
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CC The present sequence encodes a human osteoprotegerin ligand (OPGL).

CC Osteoprotegerin is a secreted member of the tumour necrosis factor creceptor family, which blocks osteoclastogenesis in a dose dependent CC manner. The OPGL protein is synthesised as a type II transmembrane CC protein. The murine and human OPGL polypeptides are 87% homologous. OPGL is a potent osteoclast differentiation factor when combined with CSF-1. CC in the not capable of inducing osteoclast differentiation in the absence CC of CSF-1. OPGL is also an activator of mature osteoclasts. The Specification describes a method for the in vivo down-regulation of CC OPGL activity in an animal. The method comprises using at least one OPGL cativity in an animal. The method and OPGL polypeptide are useful for treating, preventing and ameliorating osteoporosis or other CC diseases or conditions characterised by excessive home recommend.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 12
AAZ99964
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hypercalcaemia; osteoclas
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                                                                                                                                                                                                                                                                                                    Paget's disease;
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                                                                                                                                                                                                                                                                                                                                   osteoclast differentiation
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Query Match Best Local Similarity Matches 1285;

57.6%; 78.1%;

Score 939.6; DB 19; Pred. No. 2.2e-237; 0; Mismatches 314;

Indels Length

Gaps

11;

2274; 47;

Conservative

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The present sequence encodes human osteoprotegerin (OPG) binding protein. CC Host cells transfected with vectors containing nucleic acid molecules concoding OPG binding protein are used to produce recombinant OPG binding protein. OPG binding protein is used in binding assays to determine cc protein. OPG binding protein is used in binding assays to determine cc planting agents (particularly agonists and antagonists, including continuing cc intracellular proteins); to raise Ab (useful in immunoassays for cc detection of OPG binding protein) and to identify compounds that modulate binding of OPG binding protein to osteoclast differentiation cc and activation receptor (ODAR). The nucleic acid molecule encoding CC binding protein can be used to detect OPG binding protein-encoding CC sequences, e.g. screening for related sequences, also to produce transgenic animal models, while complementary sequences are used for CC opg binding protein, particularly soluble forms of OPG binding protein complementary sequences are used for OPG binding protein, particularly soluble forms of OPG binding protein complementary sequences are used to treat or prevent bone diseases, e.g. osteoporosis, cc disease, periodontal disease, osteoporosis, loosening of prostheses, optionally in combination with agents that promote bone growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Fig 4; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid encoding osteoprotegrin binding protein - useful for, e.g. treating bone diseases by modulating osteoclast differentiation
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16-APR-1997;
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Sequence 2274 BP; 658 A; 463 C; 523 G; 630
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CAGGAGCTCCAGCTATGATGGAAGGCTCATGGTTGGATGTGGCCCAGCGAGGCAAGCCTG
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                                          aggcctttcaaggagctgtgcaaaaggaattacaacatatcgttggatcacagcacatca
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                                                                                                 acacaactctggagagtcaagatacaaaattaatacctgattcatgtaggagaattaaac
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ttatataatatctaaagttatatttcagatgtaatgttttctttgcaaagtattgtaaat
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                   an osteoclastogenesis inhibitory factor (OCIF) binding molecule (OBM). The protein promotes and supports the separation and maturation of osteoclasts in the presence of bone absorption factors such as calcitriol or parathyroid hormone (PTH). OBM is isolated from stroma cells cultured in the presence of a bone absorption factor by separation and solubilisation of membrane proteins then affinity chromatography using OCIF. It exists in a full-sequence form and a solubilised form (sOBM) which is a shorter Chain. OBM may be used for screening potential inhibitors and modifiers of its biological activity, and screening for receptors to OBM which mediate its function. These substances can then be used in the treatment of disorders of bone function and calcium metabolism. The antibodies can be used for assay of the protein, for investigative and diagnostic purposes, and as
                                                                                                                                                                                                                                                                                                                                                                                                  02-DEC-1997;
15-APR-1997;
09-JUN-1997;
12-AUG-1997;
21-AUG-1997;
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Nakagawa
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                                                                                                                                                                                                                      Disclosure; Pages 116-117; 151pp; Japanese
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va N, Shima N,
a N, Yamaguchi
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i K, Yano K, Y
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K, Tomoyasu A,
Yasuda H;
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                                     GGCATCATGAAACATCGGGAAGCGTACCTACAGACTATCTTCAGCTGATGGTGTATGTCG
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                                                                                                                                                                                     parathyroid
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                                                                                   1; Page 15;
                                                                                             preparation
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                                                                                                                           BRAND MILK PROD
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factor; vitamin D3;
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The present invention describes a genomic DNA encoding a protein having an activity of supporting or promoting differentiation and maturation of osteoclasts. The genomic DNA encoding a protein has the following properties: (a) combines specifically with osteoclastogenesis inhibitory factor (OCIF) and has a high affinity; (b) shows a molecular weight (mw) of 30,000 to 40,000 by SDS-PAGE (sodium dodecyl sulfate-polyacrylamide gel electrophoresis) under a nonreductive condition and the apparent mw when crosslinked with monomer type OCIF is 90,000 to 110,000; and (c) has an activity of supporting or promoting differentiation and maturation of osteoclast in the co-culture of mouse osteoblast-like stroma cell and comouse spleen cell in the presence of a bone absorption promoting factor such as active type vitamin D3 and parathyroid hormone (PTH). The protein can be used as a drug and a research reagent. The present sequence cencodes a mouse OCIF binding molecule (OBM) from the present invention. Sequence 951 вP; 231 A; 267 Ç 248 <u>ი</u> 205 T; 0 other;

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Query Match
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Matches 886
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Pred. No. 2.8e
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                                                                  ACTCGACTCTGGAGAGTGAAGACACACTACCTGACTCCTGCAGGAGGATGAAACAAGCCT
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ALIGNMENTS

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Sequence 10, Application US/08996139

Patent No. 6017729

GREERAL INFORMATION:

APPLICANT: Gallbert, Laurent
APPLICANT: Gallbert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
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STREET: 51 Un:
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
                       CHORESSEE: LIBERTY 51 University
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Query Match
Best Local Similarity
Matches 1630; Conserv
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MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/95,659
FILING DATE: 22 DECEMBER 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                           08-995-659-10
                                                                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Mus musculus
IMMEDIATE SOURCE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEPAX: (206)233-0644
TREPORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: CU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patticia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852
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APPLICATION NUMBER: USSN
FILING DATE: 23 DECEMBER
CLASSIFICATION:
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                                  241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1630 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                           LIBRARY:
                              ACTCGACTCTGGAGAGTGAAGACACACTACCTGACTCCTGCAGGAGGATGAAACAAGCCT
                                                                                                                                               TCTGCAGCATCGCTCTGTTCCTGTACTTTCGAGCGCAGATGGATCCTAACAGAATATCAG
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14 OCTOBER 1997
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US-09-215-649A-10
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GENERAL INFORMATION:
                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US/09/215,649A
FILING DATE: 17-Dec-1998
                                           MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anno
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 28/
TELECOMMUNICATION INFORMATION:
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TITLE OF INVENTION: Receptor Activator of NF-kappaB
             IMMEDIATE SOURCE:
LIBRARY: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER
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                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 08/996,139
FILING DATE: <Unknown>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.
SOFTWARE: Microsoft Word for Power Macintosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Seattle
STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: <Unknown>
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CLONE: RANKL
                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                              TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
                                                                                                                             TOPOLOGY: linear
                                                                                                                                                                               LENGTH: 1630 base pairs
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          CACCCGCCGCCTCCCGCTCCATGTTCCTGGCCCTCCTGGGGCTGGGACTGGGCCAGGTGG 120
                                                  CCGGCGTCCCACACGAGGGTCCGCTGCACCCCGCGCCTTCTGCACCGGCTCCGGCGCCGC
                                                                                                                    Score 1630;
Pred. No. 0;
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                                                                                                                        Sequence 6, Application US/08842842 Patent No. 5843678 GENERAL INFORMATION:
      ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91230-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, VE
CURRENT APPLICATION DATA:
                                                                                                  APPLICANT: Boyle, WITITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                          CORRESPONDENCE ADDRESS:
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                                                                                                                  Boyle, William
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; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 158..1105
US-08-842-842-6
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A--
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 2295 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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Best Local Similarity
Matches 1629; Conserv
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                                                        ACGGAAAACTAAGGGTTAACCAAGATGGCTTCTATTACCTGTACGCCAACATTTGCTTTC
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                                     APPLICANT: Boyle,
                                                   Sequence 1, Application US/09052521C Patent No. 6316408
APPLICANT: Boyle, William J.

TITLE OF INVENTION: Osteoprotegerin Binding FILE REFERENCE: A-451Brv
CURRENT APPLICATION NUMBER: US/09/052,521C
CURRENT FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 08/880,855
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; TYPE: DNA; ORGANISM: MOUSE; FEATURE; NAME, KEY: CDS; LOCATION: (158)..(1105); US-09-052-521C-1
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TCCGAGCTGGTGAAGAAATTAGCATTCAGGTGTCCAACCCTTCCCTGCTGGATCCGGATC
                              TTAAAACCAGCATCAAAATCCCAAGTTCTCATAACCTGATGAAAGGAGGAGGAGCACGAAAA
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Sequence 1, Application US/08989362
Patent No. 6242586
GENERAL INFORMATION:
APPLICANT: Gorman, Daniel M.
APPLICANT: Matteon, Jeanine D.
TITLE OF INVENTION: Mammalian Cell Surf
TITLE OF INVENTION: Reagents
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
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STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, VG
CURRENT APPLICATION NUMBER: US/08/989,362
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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                                     TAGTATTTGATTCAAAATATTTAAAAATGTCTCACTGTTGACATATTTAATGTTTTAAAT
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                  GGCAGAATACTGTTTCTGGTGACCACATGTAGTTTATTTCTTTATTCTTTTTAACTTAAT
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US-09-052-521C-3
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TITLE OF INVENTION: Osteoprotegerin Binding Pr
FILE REFERENCE: A-451Brv
CURRENT APPLICATION NUMBER: US/09/052,521C
CURRENT FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 08/880,855
PRIOR APPLICATION NUMBER: 08/842,842
PRIOR APPLICATION NUMBER: 08/842,842
PRIOR FILING DATE: 1997-04-16
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SOFTWARE: PatentIn Ver.
SEQ ID NO 3
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Best Local
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TYPE: DNA
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                                                                              AGGCCCAGCCATTTGCACACCTCACCATCAATGCTGCCAGCATCCCATCGGGTTCCCATA 474
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TAAGCAACGGAAAACTAAGGGTTAACCAAGATGGCTTCTATTACCTGTACGCCAACATTT
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Pred. No. 4.5e-247;
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 954 base pairs
LENGTH: nucleic acid
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US-08-996-139-12
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                                                                                                                                                                                                                                            CLONE:
FEATURE:
                                                                                                                                                                                                                                                                                            URGANISM: Homo sapiens
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 28 TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: 1
FILING DATE: 14 OCTOR
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy
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OPERATING SYSTEM: Apple Operating System
SOFTWARE: Microsoft Word for Power Macint
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                      NAME/KEY:
       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Perkins, Patricia Anne REGISTRATION NUMBER: 34,693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/996,139 FILING DATE: 22 DECEMBER 1997 CLASSIFICATION:
                                                                                                                                                                                                                                                                                  LIBRARY:
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(206)233-0644
                                                                                       Conservative
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14 OCTOBER 1997
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                                                                                   Score 615; DB 3;
Pred. No. 1.4e-158;
0; Mismatches 150;
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US-08-995-659-12

STREET:
CITY: Se
STATE: W
COUNTRY:

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Sequence 12, Application US/08995659 Patent No. 6242213 GENERAL INFORMATION:
                                                                                                                               APPLICANT: Anderson, Dirk M. APPLICANT: Galibert, Laurent APPLICANT: Maraskovsky, Eugene
                                                                               CORRESPONDENCE ADDRESS:
                                                                                              TITLE OF INVENTION: Ligand for Receptor Activator NUMBER OF SEQUENCES: 19
                              CACCGGCGCCTCCGGCTCCATGTTCCTGGGCCTCCTGGGGCTGGGACTGGGCCAGGTGG
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              Seattle
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                                                                 Immunex Corporation, Law Department
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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HYPOTHETICAL: N
ANTI-SENSE: NO
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MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.
SOFTWARE: Microsoft Word for Power Macintosh
CURRENT APPLICATION DATA:
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APPLICATION NUMBER: USSN
FILING DATE: 23 DECEMBER
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CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
USSN 60/064,671
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NAME: Perkins, Patricia
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CLONE: }
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LOCATION:
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                                                                                                                                                          TCTGCAGCATCGCTCTGTTCCTGTACTTTCGAGCGCAGATGGATCCTAACAGAATATCAG 180
                                                                                                            AAGACAGCACTCACTGCTTTTATAGAATCCTGAGACTCCATGAAAACGCAGATTTGCAGG 240
                       ACTCGACTCTGGAGAGTGAAGACAC-----ACTACCTGACTCCTGCAGGAGGATGAAAC 294
                                                                                          nucleic acid
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Pred. No. 1.4e-158;
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Patent No. 6271349
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
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                                                                                                                                COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power MacIntosh
OPERATING SYSTEM: Apple Operating System 7.5.
SOFTWARE: Microsoft Word for Power MacIntosh
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                      Gallbert, Laurent
Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                         APPLICATION NUMBER: US/09/215,649A
FILING DATE: 17-Dec-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
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              APPLICATION NUMBER: 08/996,139
FILING DATE: <UNKNOWN>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
                                                                                                                                                                                                                               ADDRESSEE: Immunex Corporation, STREET: 51 University Street CITY: Seattle STATE: WA COUNTRY: USA ZIP: 98101
NUMBER: USSN 08/772,330
                                                                                                                                                                                                                                                                                                         Law Department
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; LOCATION: 1..951
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CCGGCGTCCCACACGAGGGTCCGCTGCACCCGCGCCTTCTGCACCGGCTCCGGCCCCGC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
LIBRARY: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: cDNA HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 23 DECEME ATTORNEY/AGENT INFORMATION:
                        TAAGCAACGGAAAACTAAGGGTTAAACCAAGATGGCTTCTATTACCTGTACGCCAACATTT
                                                                                     AAGTCACTCTGTCCTCTTGGTACCACGATCGAGGCTGGGCCAAGATCTCTAACATGACGT
                                                                                                                                                                                                          CAGGAGCTCCAGCTATGATGGAAGGCTCATGGTTGGATGTGGCCCCAGCGAGGCAAGCCTG
                                                                                                                                                                                                                                                                                                                                                                                              AAGACAGCACTCACTGCTTTTATAGAATCCTGAGACTCCATGAAAACGCAGATTTGCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCTGCAGCATCGCTCTGTTCCTGTACTTTCGAGCGCAGATGGATCCTAACAGAATATCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION
        TTAGCAATGGAAAACTAATAGTTAATCAGGATGGCTTTTATTACCTGTATGCCAACATTT
                                                                                                                                                GAGCAGAGAAAGCGATGGTGGATGGCTCATGGTTAGATCTGGCCAAGAGGAGCAAGCTTG
                                                                                                                                                                                                                                                    AGGCCTTTCAAGGAGCTGTGCAAAAGGAATTACAACATATCGTTGGATCACAGCACATCA
                                                                                                                                                                                                                                                                     AAGCCTTTCAGGGGGCCGTGCAGAAGGAACTGCAACACATTGTGGGGCCCACAGCGCTTCT
                                                                                                                                                                                                                                                                                                                                 ACTCGACTCTGGAGAGTGAAGACAC-----ACTACCTGACTCCTGCAGGAGGATGAAAC
                                                                                                                              AAGCTCAGCCTTTTGCTCATCTCACTATTAATGCCACCGACATCCCATCTGGTTCCCATA
                                                                     AAGTGAGTCTGTCCTTGGTACCATGATCGGGGGTTGGGCCAAGATCTCCAACATGACTT
                                                                                                                                                                                                                                                                                                                 ACACAACTCTGGAGAGTCAAGATACAAAATTAATACCTGATTCATGTAGGAGAATTAAAC
                                                                                                                                                                                                                                                                                                                                                                              AAGATGGCACTCACTGCATTTATAGAATTTTGAGACTCCATGAAAATGCAGATTTTCAAG
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLONE: huRANKL (full length)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Perkins, Patricia REGISTRATION NUMBER: 34,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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82.2%;
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Pred. No. 1.4e-158;
0; Mismatches 150;
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US-09-320-424-10
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; LOCATION: (1)..(759)
US-09-320-424-10
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EARLIER FILING DATE: 1998-03-26
EARLIER APPLICATION NUMBER: 08/670,354
EARLIER FILING DATE: 1996-06-25
EARLIER FILING DATE: 1996-06-25
EARLIER APPLICATION NUMBER: 08/548,368
EARLIER FILING DATE: 1995-11-01
EARLIER APPLICATION NUMBER: 08/496,632
EARLIER FILING DATE: 1995-06-29
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
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Patent No. 6284236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 10
LENGTH: 759
                                                                                                                                                                                                                                                                                       Matches 174;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/320,424
CURRENT FILING DATE: 1999-05-26
EARLIER APPLICATION NUMBER: 09/190,046
EARLIER FILING DATE: 1998-11-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Wiley, Steven R.
APPLICANT: Goodwin, Raymond G.
TITLE OF INVENTION: Cytokine that Induces Apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 2835-E
                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: synthetic fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
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                                                                                                                                                                                                                                 525 AACATGACGTTAAGCAAACGGAAAACTAAGGGTTAACCAAGATGGCTTCTATTACCTGTAC 584
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTAAGTTACGGTCTGGAGAGGAAATCAGCATCGAGGTCTCCAACCCCTCCTTACTGGATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCAAGTATTGGTCAGGGAATTCTGAATTCCATTTTATTCCATAAACGTTGGTGGATTTT
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                                                                                                                                                                                                            aacttgcacttgaggaatggtgaactggtcatccatgaaaaagggttttactacatctat 471
agtgctagaaatagttgttggtctaaagatgcagaatatggactctattccatctatcaa
                                   GGAGGGAGCACGAAAAACTGGTCGGGCAATTCTGAATTCCACTTTTATTCCATAAATGTT 764
                                                                       caaatggtccaatatatttacaaatacacaagttatcctgaccctatattgttgatgaaa
                                                                                                       CTGATGGTGTATGTCGTTAAAACCAGCATCAAAATCCCAAGTTCTCATAACCTGATGAAA 704
                                                                                                                                         tcccaaacatactttcgatttcaggaggaa---ataaaagaaaacacaaagaacgacaaa 528
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                                                                                                                                                                                                                                                                                                          3.6%;
50.0%;
                                                                                                                                                                                                                                                                                       Score 58.4; DB 4;
pred. No. 1.6e-06;
0; Mismatches 171;
                                                                                                                                                                                                                                                                                                                               Length 759;
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NAME/KEY: CDS
LOCATION: (1)..(768)
US-09-320-424-12
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EARLIER APPLICATION NUMBER: 09/190,046
EARLIER FILING DATE: 1998-01-10
EARLIER FILING DATE: 1998-11-10
EARLIER FILING DATE: 1998-03-26
EARLIER FILING DATE: 1998-03-26
EARLIER APPLICATION NUMBER: 08/670,354
EARLIER FILING DATE: 1996-06-25
EARLIER APPLICATION NUMBER: 08/548,368
EARLIER APPLICATION NUMBER: 08/548,368
EARLIER FILING DATE: 1995-11-01
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LENGTH: 768
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 3.6%;
Best Local Similarity 50.0%;
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APPLICANT: Goodwin, Raymond G.
TITLE OF INVENTION: Cytokine that Induces Apoptosis
FILE REFERENCE: 2835-E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Ver. 2.0
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EARLIER FILING DATE: 1995-06-29
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                                                                                                                                                                                                                                                                                                                                                                                                                         aacttgcacttgaggaatggtgaactggtcatccatgaaaaagggttttactacatctat 480
                                                                                                                                                                                                                                                                                             CTGATGGTGTATGTCGTTAAAACCAGCATCAAAATCCCAAGTTCTCATAACCTGATGAAA 704
                                                                                                                                                                    agtgctagaaatagttgttggtctaaagatgcagaatatggactctattccatctatcaa
                                                                                                                                                                                               GGAGGGAGCACGAAAAACTGGTCGGGGCAATTCTGAATTCCACTTTTATTCCATAAATGTT 764
                                                                                                                                                                                                                                                      caaatggtccaatatatttacaaatacacaagttatcctgaccctatattgttgatgaaa 597
ttgatagacatggaccatgaagccagttttttcggggcctttttagtt 765
                                       CTGCTGGATCCGGATCAAGATGCGACGTACTTTGGGGGCTTTCAAAGTT 872
                                                                                   gggggaatatttgagcttaaggaaaatgacagaatttttgtttctgtaacaaatgagcac
                                                                                                                             GGGGGATTTTTCAAGCTCCGAGCTGGTGAAGAAATTAGCATTCAGGTGTCCAACCCTTCC 824
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 58.4; DB 4;
Pred. No. 1.6e-06;
0; Mismatches 171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 768;
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RESULT

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US-08-780-496-2

; Sequence 2, Application US/08780496

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; LENGTH: 1042
; TYPE: DNA
; ORCANISM: Homo sapiens
US-08-584-031-2
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APPLICANT: AShkenazi, Avi J.
TITLE OF INVENTION: APO-2 LIGAND
FILE REFERENCE: 11669.22US03
CURRENT APPLICATION NUMBER: US/08/584,031A
CURRENT FILLING DATE: 1996-01-09
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PATENTIN VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 3.6%;
Best Local Similarity 50.0%;
Matches 174; Conservative
                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: AV1 AS
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                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
             ATTORNEY/AGENT INFORMATION: NAME: Marschang, Diane L
                                                                                                                                                                                                                                          APPLICANT: Avi Ashkenazi, Anan Chuntharapai, Kyung Jin Kim
TITLE OF INVENTION: Apo-2 Ligand
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       883 ttgatagacatggaccatgaagccagttttttcgggggcctttttagtt 930
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                                                           APPLICATION NUMBER: US/08/780,496 FILING DATE: 08-Jan-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        585 GCCAACATTTGCTTTCGGCATCATGAAACATCGGGAAGCGTACCTACAGACTATCTTCAG 644
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                                                CLASSIFICATION:
                                                                                                                                                                                                                              COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1042;
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                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Mcintosh
OPERATING SYSTEM: Apple 7.5.2
SOFTWARE: Microsoft Word, Version 6.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/670,354
FILING DATE: 25-JUN 1996
CLASSIFICATION: 435
         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/496,632
FILING DATE: 29-JUN-1995
                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS
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STREET: 51
Seattle
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
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E: Kathryn A. Anderson, 51 University Street

Immunex Corporation

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US-08-670-354-3
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                                                                                                    Sequence 3, Application US/08670354
Patent No. 5763223
GENERAL INFORMATION:
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Best Local Similarity 50.0%;
Matches 174; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1042 base pair
APPLICANT: Steven R. Wiley and APPLICANT: Raymond G. Goodwin.
TITLE OF INVENTION: Cytokine That Induces Apoptosis NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: POSTELECOMMUNICATION INFORMATION: TELEPHONE: 415/225-5416
TELEPHONE: 415/952-9881
                                                                                                                                                                                                                                                          883 TTGATAGACATGGACCATGAAGCCAGTTTTTTCGGGGCCTTTTTAGTT
                                                                                                                                                                                                                                                                                          825 CTGCTGGATCCGGATCAAGATGCGACGTACTTTGGGGCTTTCAAAGTT 872
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TYPE: Nucleic Acid
STRANDEDNESS: Single
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Pred. No. 1.9e-06;
0; Mismatches 171;
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HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: HUAIC-dv
FEATURE:
HAME/KEY: CDS
LOCATION: 78..383
US-08-670-354-3
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TELEX: 756822
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1521 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 3.6%; Score 58.4; DB 1; Length 1521; Best Local Similarity 50.0%; Pred. No. 2.3e-06; Matches 174; Conservative 0; Mismatches 171; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/548,368
FILING DATE: 01-NOV-1995
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/ACENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REGISTRATION NUMBER: 2835-B
TELECOMMUNICATION INCREMATION:
TELEPHONE: (206) 587-0430
TELEPHONE: (206) 533-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: NO. STRANDEDNESS: Single TOPOLOGY: linear MOLECULE TYPE: cDNA to mRNA MOLECULE TYPE: NO.
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542 CARATGGTCCAATATATTTACAAATACACAAGTTATCCTGACCCTATATTGTTGATGAAA 601
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Search completed: July 8, 2002, 20:04:31 Job time: 710 sec

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Result
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Maximum Match 100%
Listing first 45 s
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Perfect score:
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              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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length: 2000000000
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              July 8, 2002, 20:04:46; Search time 2842.81 Seconds (without alignments) 7738.835 Million cell updates/sec
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Gapop 10.0 , Gapext 1.0
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1630
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AA170348 ms88g11.r
AQ827168 Hs_5256_B
AG107545 Pan trog1
AA504450 aa59h12.r
AV653073 AV653073
AZ834036 ZM0116604
AQ817650 HS_5265_B
BG206347 RST25278
BG206447 RST25278
BG21644205 RST3126 A
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BE335979 us84g09.y
AQ827122 HS_5256_B
AQ417854 RPCI-11-1
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KEYWORDS
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AW104819	CNS07A2Y	CNS0072R	CNS029ER	CNS00KAE	BG712984	CNS04D0K	CNS04E5M	BM440311	CNS01090	BG216814	CNSOOETW	CNS04P4P	вм358116	CNS015WU	CNS00EVL	AL543620	AL547417	AW945165	AW949689	BE042463	CNS00DKY	CNS0039G	BG016736	CNS00FMC	BG212237	BG197160	BF427340
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DEFINITION
CH330-186C1, DNA sequence.
ACCESSION
WERSTON
BH267783.1 GI:17180093
KEYWORDS
SOURCE
ORGANISM
Rattus norvegicus
Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
And Gesses 1 to 612)
AUTHORS
A., Gebregeorgis, E., Overton, L., Russeli, D., Chen, D., Riggs, F., de
JODG, P. and Fraser, C.M.
TITLE
JOURNAL
JOURNAL
UNDUBLISHED (1999)
Cher_GSS: CH230-186C1.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomics
The Institute for Genomic Research
PAx: 301 838 0200
Fax: 301 838 0200
Fax: 301 838 0200
Fax: 301 838 0200
Fax: 301 838 0200
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejongémail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering.information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Seq primer: T7
Class: BAC ends.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                            AATGGATGATGTCTATACATGTGTAAGACTACTAAGAGACATGGCCCACGGTGTATGAAA 1004
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                                                                                                                                                                                                                                                                                                                                                                                                                                CTGTTGGATCCGGATCAAGATGCGACGTACTTTGGGGGCTTTCAAAGTTCAAGACATAGAC
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                                                                                                                                      BB223942 RIKEN full-length enriched, adult male aorta and vein Mus musculus cDNA clone A530084G16 3' similar to AF019048 Mus musculus receptor activator of nuclear factor kappa B ligand (RANKL) mRNA,
                                                                                   EST
                                                                                                               mRNA sequence.
BB223942
Arakawa, T.,
                                         Eukaryota; Metazoa;
                                                      Mus musculus
                                                                                                 BB223942.2
                            Mammalia; Eutheria;
                                                                       nouse mouse
             (bases 1 to 469)
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/cell_type="Brain"
/notte="Vector: pTARBAC2.1; Sit
CHORI-230 Rat (BN/SSNH5d/MCW)
Pieter_de_Jong"
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/clone="CH230-186C1"
/clone_11b="CHORI-230 Segment 1"
Carninci, P.,
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91.6%;
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Sciurognathi;
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URL:http://genome.gsc.riken.go.jp/

Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)

wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
hayashizaki,Y.
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Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              encyclopedia: real-time sequence clustering for construction of nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aiz,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and Hayashizaki,Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            On Jul 1, 2000 this sequence v
Contact: Yoshihide Hayashizaki
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Encyclopedia Project of Genome Exploration Research Gro
Genomic Sciences Center and Genome Science Laboratory i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RÎKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome 10 (11), 1757-1771 (2000) Konno, H., Fukunishiy., Shibata, K., Itoh, M., Carninci, P., Sugrand munchischiy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Division of Experimental Animal Research in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Please visit our web site (http://genome.gsc.riken.go.jp/) further details.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mouse tissues
prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                       contributed to prepare
                                                                                                                                                                                                                                                                                                                                                                                               /note="Site_1: SalI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="male"
/tissue_type="aorta and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and vein"
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/clone="A530084G16"
/clone_lib="RIKEN full
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1. .469
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                                                         Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
2E 1 (bases 1 to 475)
2E 1 (bases 1 to 475)
2E 1 (bases 1 to 475)
3E 1 (bases 1 to 475)
4. Koya.S., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.,M., Koya.S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,
4. Koya.S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,
5. Okazaki,Y., Okido,T., Saito,R., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
7agami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
Muramatsu,M. and Hayashizaki,Y.
8. RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
4. Contact: Yoshihide Hayashizaki
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research (RIKEN)
7-7-2 Snehiro-cho. Tsurumi-ku. Yokohama Kanagawa 230-0045, Japan
1-7-2 Snehiro-cho. Tsurumi-ku. Yokohama, Kanagawa 230-0045, Japan
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BB637568 BB637568.1 GI:1647374'2
                     1-7-22 Suehiro-cho, Tsurumi-ku, Tel: 81-45-503-9222 Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
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genome-res@gsc.riken.go.jp,
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CTGGGACCTGCAAATAAGTTCTTTTTTTCTAATGAGGAGAGAAAAATATATGTATTTTTA 1369
                                                                                                              ATGTCATTGCAAAGAAATGATAGTGTGAAGGGTTAAGTTCTTTTGAATTGTTACATTGCG 1309
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                                                                                                                                                                                                                                                                              441;
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RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Please visit our web site (http://genome.gsc.rlken.go.jp) for further details.
e mouse tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
                                                                                                                                                                                                                                                                                                   Similarity
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/clone_lib="RIKEN full-length enriched, adult male aorta
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/db_xref="taxon:10090"
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5', mRNA sequence.
BE633100
BE633100.1 GI:9915788
EST.
                                                                                                                                                                                                                                                                                                                                                                 Tumor Gene Index Unpublished (1997) Unpublished (1997) Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the Thack Consortium (info@lmage.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; 1 (bases 1 to 482)
NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Pro
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                                                                                                                                                                                                                                                                                                                    quality sequence stop: Location/Qualifiers
                                                      /tissue_type="Spleen"
/dev_stage="4 weeks"
/lab_host="DH10B"
                                                                                                                                                                                                                                                        /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:3412782"
                                                                                                                                                                                                                                /sex="male"
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EST.
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free tl
IMAGE Consortium (info@image.llnl.gov)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:3325120"
/clone_lib="Soares mouse 3
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/dev_stage="4 weeks"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genomic (
                                                                                                      library availability, please contact Pleter de Jong (pleter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering.bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu plate: 832 row: F column: 18
                                                                          Seq primer: T7
Class: BAC ends
                                                                                                                                                                                                                                  High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, Tel: (206) 616-3618

Fax: (206) 616-3887
                                                                                                                                                                                                                                                                                                                                              scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96
                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 524)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AQ827122.1
GSS.
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                                                                                                                                                                                                   Clones are derived from the human BAC library RPCI-11. For BAC
                                                                                                                                                                                                                                                                                                                Contact: Mahairas GG, Wallace JC,
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milarity 100.0%;
Conservative 0
                                           quality sequence stop: 524.
Location/Qualifiers
                                                                                                                                                                                                                   jwallace@u.washington.edu
/organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                       AQ417854
AQ417854.1
Unpublished (1997)
Other_GSSs: RPCI-11-185M9.
Contact: Shaying Zhao, Wil
                                                                            Mammalia; Eutheria; 1 (bases 1 to 575) Zhao, S., Adams, M.D.,
                                                                                                                                             human.
                                                                                                                                                                                                   DNA sequence.
                                                                                                                                                                                                               RPCI-11-185M9.TV
                                        Map Building
                                                      Use of BAC End
                                                                                                                 Eukaryota;
                                                                                                                                  Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: pBACe3.6; Site_1: ECORI; Site_2: ECORI; Male blood DNA was isolated from one randomly chosen do and partially digested with a combination of ECORI and ECORI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at ECORI sites"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="Plate=832 Col=18 Row=F"
/clone_lib="RPCI-11 Human Male BAC Library"
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Primates;
                                                                             Nierman, W.,
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Pred. No. 7.6e-45;
0; Mismatches 123;
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genomic clone
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                                                                                                                                                                                                                                                GTCTTGCTGTTGACATATTTAATGTTTTAAATGTTACAGACATATTTAACTGGTGCACTTT
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                                                                                              CAAATGCAGTATATTTCTTCATTCTTTTAAGTTAATAGATTTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genet cs (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
seq primer: T7
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The Institute for Genomic Research
9712 Medical Center Dr., Rockville
 AA170348
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/cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI;
/note="Vector: pBACe3.6; Site_1: EcoRI;
RPCII1 Human Male BAC Library"
a 79 c 120 g 198 t
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/clone="RPCI-11-185M9"
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75.4%;
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Pred. No. 9.8e-42;
0; Mismatches 102;
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TGACCACATGTAGTTTATTTCTTTATTCTTTTAACTTAATAGAGTCTTCAG
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Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 530)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WashU-HHMI Mouse EST Project Washington University School of MedicineP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1996)
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                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                          /tissue_type="Spleen"
/dev_stage="4 weeks"
/lab_host="DH10B"
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Soares
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                                                                                                                                                                                                                                                                    14.0%;
99.1%;
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Pred. No. 9.3e-38;
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                                                                                                                                                                                                                                                                        676 AAATCCCAAGTTCTCATAACCTGATGAAAGGAGGAGGAGCACGAAAAACTGGTCGGGCAATT 735
                                                                                                                 796
                                                                                                                                                                                                         736
TTGGGGCTTTCAAAGTTCAGGACATAGACTGAGACTCATTTCGTGGAACATTAGCATGGA
                                                                                          AAATTAGCATTCAGGTGTCCAACCCTTCCCTGCTGGATCCGGATCAAGATGCGACGTACT
                                                                                                                                                                                  CTGAATTCCACTTTTATTCCATAAATGTTGGGGGATTTTTCAAGCTCCGAGCTGGTGAAG 795
                                                                                                                                                                                                                                                AAATCGCAAGTTCTCATACCNTGATGAAAGGAGCAAGCACCAAGTATTGGTCAGGGAATT 408
                                                                                                                                                        CTGAATTCCATTTTTATTCCATAAACGTTGGTGCATTTTGTAAGTTACGGTCTGGAGAGG
                                                                   AAATCAGCATCGAGGTCTCCAACCCCTCCTTACTGGATCCGGATCAGGATGCAACATACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High Throughput Sequencing Center University of Washington 401 Queen Anna Anna Anna Center 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence stop: 529
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            401 Queen Anne Avenue North, Seattle, WA 98109, Tel: (206) 616-3618
Fax: (206) 616-3887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seq primer: T7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          147
                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI wale blood DNA was isolated from one randomly chosen and partially digested with a combination of EcoRI an EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"

a 121 c 102 g 153 t 6 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="plate=832 Col=18 Row=N"
/clone_lib="RPCI-11 Human Male E
/sex="male"
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Pred. No. 1.1e-37;
0; Mismatches 115; Indels 11;
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Adams,M.D.
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CTTCTCCACAGGTTCCCATAAAGTGAGTCTGTCCTCTTGGTACCATGATCGGGGTTGGGC 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGGTTTTACAATTTTGTAATGATTTCCTAGAATTGAACCAGA 1129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGTCCTAGATGTTTGGAAACTTCTTAAAAA-----ATGGATGATGTCTATACATGTGT 968
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGGTTTGTAGATTNTGTAAGNAGTACTAACGACTGCAACAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9117], Fax:81-45-503-9170;
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fujiyama,A., Hattori,M., Toyoda,A., Totoki,Y., Watanabe,H. and Sakaki,Y. BAC end sequences of Library PTB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GSS; GSS (genome survey sequence).
Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male BAC Library clone:PTB-112G09.F.
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Pan troglodytes DNA, clone: PTB-112G09.F, genomic survey sequence.
AG107545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fujiyama, A., Hattori, M., To
Totoki, Y., Watanabe, H. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                clone tracking errors.
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                                                                                      Similarity
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R.Site 2
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                                                                                                                                                                         /cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
168 c 121 g 189 t
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/clone="PTB-112G09.F"
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1. .659
                                                                                                                                                                                                                                     /sex="male"
                                                                                                                                                                                                                                                                                    /organism="Pan troglodytes"
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Primates;
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Pred. No. 7.7e-33;
Pred. No. 7.7e-33;
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aa59h12.rl NCI_CGAP_GCB1
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                                                                                                                                                                                                                                                                                                                             cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -28ml3 revl ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                               Bonaldo, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.,
Ph.D., Gerald Marti, M.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tumor Gene Index
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National Cancer Institute, Cancer Genome Anat
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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(bases 1 to 419)
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Location/Qualifiers
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                                                                                         constructed by Bento Soares and M. Fatima Bonaldo." 58\ c 96\ g 144\ t
                                   (Pharmacia), digested with Not I and cloned into and Eco RI sites of the modified pT773 vector. Li went through one round of normalization, and was
                                                                                                                                                                                                                                                /db_xref="taxon:9606"
/clone="IMAGE:825287"
                                                                                                                                                                                                        /tissue_type="germinal center B cell"
/lab_host="DH10B"
                                                                                                                                                                                                                                  /clone_lib="NCI_CGAP_GCB1"
                                                                                                                                                                                                                                                                           ∕organism="Homo sapiens"
                                                                              Double-stranded cDNA was ligated to Eco RI adaptors
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1013 CCTCTCTTGAGCCTGTACAGGTTGTGTATATGTAAAGTCCATAGGTGATGTTAGATTC 1072
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Insight into hepatocellular carcinogenesis at transcriptome level
                                                                                                                                                                                                                                         Chinese National Human
351 Guo Shoujing Road,
201203, P. R. China
                                                                                                                                                                                                                                                                                                                                                      by comparing gene expression profiles of hepatocellular with those of corresponding noncancerous liver proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
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EST.
                                                                                                                                                      This
                                                                                                                                                                                                                         Tel: 86-21-50801919(ex.45)
                                                                                                                                                                                                                                                                                                                 Contact: Zeguang Han
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 362)
                                                                                                                                                      l: hanzg@chgc.sh.cn
clone is available
                                                                                                                                                                                                    86-21-50801922
/clone="GLCDHB01"
/clone_lib="GLC"
/tissue_type="corresponding non
                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                               Location/Qualifiers
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Zhangjiang Hi-Tech Park, Pudong, Shanghai
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301 3', mRNA sequence.
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                                                                                                    Rm. 30
84112,
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0116 row: G column: 04
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                     Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                         Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                            Mouse whole genome scaffolding with paired end
                                                                                                                                                                                                                Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                         618 bp DNA linear GSS 20-FEB-20. 2M0116C04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0116G04 R, DNA sequence. A2834036
                                                                                                                                                                     Unpublished (2000)
                                                                                                                                                                                    plasmid inserts
                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                  Mus musculus
                                                                                                                                                                                                                                                                                                                                house mouse.
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/lab_host-"SOLR"
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                                                                                                                                                                                                                                     TITLE
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                                                                                                                                                                JOURNAL
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  267 CTACCTGACTCCTGCAGGAGGATGAAACAAGCCTTTCAGGGGGGCCGTGCAGAAGGAA 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           207
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                              Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
                                                                                                                          Sequence-tagged connectors: A sequence approach to mappin scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
High Throughput Sequencing University of Washington
                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 413)

Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Adams,M.D. and Mahairas,G.G., Wallace,J.C., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Mahairas,G.G., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Mahairas,G.G., Wallace, J.C., Smith,K., Swartzell,S., Holzman,T., Mahairas,G.G., Wallace,J.C., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Mahairas,G.G., Wallace,G., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Mahairas,G.G., Wallace,G., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Mahairas,G.G., Wallace,G., Wallace,G.,
                                                                                                                      99380589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AQ817650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with 74 DNA polymerase and 74 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWSA2 (gil473214/gb)AF129072.l), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     quality sequence stop: 618
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /lab_host="E. Coli strain xL10-Gold, T1-resistant, F
/note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:10090"
/clone="UUGC2M0116G04"
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /sex="Male"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 165.8; DB 12;
Pred. No. 1.5e-24;
0; Mismatches 7;
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sapiens
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BASE COUNT
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                                                                                                          REFERENCE
AUTHORS
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BG203357/c
                                                                                                                                                                                                                                       KEYWORDS
                                                                                                                                                                                                                                                             VERSION
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Best Local Similarity
Matches 172; Conserv
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      TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAGAAATTAGCATTCAGGTGTCCAACCCTTCCCTGCTGGATCCGGATCAAGATGCGACGT 852
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGTATTCCTGGATTGTCGGAACATTTTTAAACACGCCAGCTAGATGTTATATGTGGTGAA 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTACTA 978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGATGTCCTAGATGTTTGGAAACTTCTTAAAAAATGGATGATGTCTATACATGTGTAAGA 972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACTTTGGGGCTTCTTAAGAGCGAGATATGGATTGGGCCACACTTTTTGGAA----TGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                  CTACTA 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: jwallace@u.washington.edu
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieteredejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
plate: 841 row: H column: 5
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Tel: (206) 616-3618
Fax: (206) 616-3887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seq primer: SP6
Class: BAC ends
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 276)

Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Boozer,S., Mays,R., Smith, E., Veloso,N., Kilka,A., Hess,J., Cothren,K., Lo,K., Offenbacher,J., Danzig,J. and Ducar,M.
                                                                                                                                                                                                                                     BG203357

RST22738 Athersys RAGE Library F

BG203357

BG203357.1 GI:13725044

EST.
                                                                                                                                                                                                                   human
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Location/Qualifiers
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100 g 123 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="Plate=841 Col=5 Row=H"
/clone_lib="RPCI-11 Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 116;
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                                                                                                                                                                                                                                                                                                              Homo
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                                                                                                                                                                                                                                                                                                                                     mRNA
                                                                                                                                                                                                                                                                                                              sapiens
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                                                                                                                                                                                                                                                                                                              linear EST 21-APR-2001
s cDNA, mRNA sequence.
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Best Local :
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CCAGCCATTTGCACACCTCACCATCAGTGCCAGCATCCCATCGGGT 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)
21227151
                                                                                                                                                                                                                                                                                                                                                                                                                                                            3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
                                                                                                                                                                                                                                                                                                                                                                                                                              Email: scain@athersys.com
High quality sequence stop:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Athersys, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Scott J. Cain
                                                                                                                                           Similarity
                                                                                                                                                                                                                         92
                                                                                                                              4.4%;
|llarity 78.9%;
|Conservative
                                                                                                                                                                                                                    Libraries using Random Activation of Gene Expression, Nature Biotechnology, in press. Note that even though the Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."
                                                                                                                                                                                                                                                                                                                     /note="See 'Creation of Genome-wide Protein Expression
                                                                                                                                                                                                                                                                                                                                  /clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                 0;
                                                                                                                                Score 72.2; DB 10
Pred. No. 5.7e-05;
0; Mismatches 23
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FEATURES

Search completed: July Job time: 8768 sec 8 22:30:54

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Result
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Maximum Match 100%
Listing first 45 s
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Maximum DB
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Perfect score:
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score greater than
and is derived by a
                                                                                                                                                                                                                                                                                   Score
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seq length:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A_Geneseq_032802:*

1: /SIDS5/gcgdata/g

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This represents a murine RANKL, a ligand for the RANK (receptor cc activator of necrosis factor-kappaB (NF-kB)) polypeptide. RANK is a cc member of the tumour necrosis factor (TNF) family. A soluble RANK is a cc may be used for inhibiting activation of NF-kB, by contacting a cell cexpressing membrane-associated RANK with a soluble RANK which binds to call cexpressing membrane-associated RANK with a soluble RANK which binds to call cexpressing membrane-associated RANK with a soluble RANK which binds to call certain the composition of NF-kB, by contacting a cell certain cell sand enhance their cells and enhance their resoluble RANK polypeptide composition may also be used for regulating an immune or inflammatory response. Inhibition of NF-kB by RANK antagonists may be useful in ameliorating negative effects of an inflammatory cells creations. They can also be used in adjunct therapy for disease cells that express RANK. RANKL polypeptides can also be used to identify inhibitors of RANK and thus inhibitors of an inflammatory response, and also for protecting RANK. Pankl. polypeptides of from the negative effects of chemotherapy or the presence of high levels cells strate and also be used for detection and drug cells from the negative effects of chemotherapy or the presence of high levels cells strate products can also be used for detection and drug cells creening.
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02-JUL-1998

Murine receptor activator of

NF kappaB ligand (RANKL) protein

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23-DEC-1996;
07-MAR-1997;
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N-PSDB; AAV41371.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                294;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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anti-apoptotic

Murine; receptor activator of nuclear factor kappaB l

ligand; RANKL;
d factor; TRAF;

Immune response; inflammatory response; graft-versus-host reaction; toxic shock; sepsis; acute inflammatory reaction; bone resorption; anti-apoptotic signal; therapy; immunosuppressant; anti-inflammator

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CC Rappas (RANK) proteins and their corresponding DNAs. RANK is a member of the tumour necrosis factor (TNF) receptor superfamily and associates with TNF receptor associated factor (TNF)? and 3 which are important in the regulation of immune and inflammatory response. The receptors of immune and inflammatory response. The receptors of immune and inflammatory response. The receptors of immune and inflammatory responses. The receptors of inhibitors of these receptors. The cytoplasmic domain of RANK is used in developing assays for inhibitors of signal transduction, e.g. for screening the molecules that inhibit interaction of RANK with TRAF1, TRAF2, TRAF3, TRAF5 and particularly TRAF6. NF kappab inhibition by RANK antagonists or response that result from triggering of RANK, e.g. in treating toxic shock or sepsis, graft-versus-host reactions, acute inflammatory cresponse that result from triggering of RANK, e.g. in treating toxic shock or sepsis, graft-versus-host reactions. RANK acts as an anticomplete forms of the receptor are used in vivo or in vitro based of care in the composition of the receptor are used in vivo or in vitro based care useful not be signal via RANK. RANK compositions are used in the careful state of both agonists or antagonists of RANK activity as a sample of the receptor are used in vivo or in vitro based of care useful for modulating that interfere with RANK/TRAF6 interactions are useful for modulating that interfere with RANK/TRAF6 interactions are useful for the expression of recombinant proteins, as probes for analysis of the presence or distribution of RANK transcripts, while the proteins are useful in preparing kits for the detection of soluble RANK, or monitor RANK ligand
 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-OCT-1997;
23-DEC-1996;
07-MAR-1997;
                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New receptor activator of NF-kappaB (RANK) polypeptides, useful for regulating immune response, in screening for RANK inhibitors, or as adjunct therapy for disease characterized by neoplastic cells that express RANK -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-AUG-2001
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07-MAR-1997;
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S
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96US-0772330.
97US-0813509.
97US-0996139.
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                                                                                                      activity.
murine.
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Score
Pred.
                                                                                                                    The
                                                                                                                      present
1561; DB 22;
No. 2.4e-140;
                                                                                                                      sequence
              Length 294;
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RESULT
AAE04425
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                                                                                                                                                                                                                         23-DEC-1996;
07-MAR-1997;
14-OCT-1997;
The present invention relates to receptor activator of NF-chi B (RANK) DNA. RANK is mapped to chromosome 18q22.1 and its ligand (RANKL) to chromosome 13q14. RANK and RANKL are type 1 and type 2 transmembrane proteins respectively. RANK is a member of the tumour necrosis factor (TNF) superfamily and it closely resembles CD40 in the extracellular region. RANK associates with TNF receptor-associated factor (TRAF) 2 and TRAFF3. The DNA molecules are useful for producing ligands of RANK.
                                                                                                                                                                                                                                                                                                                                           Key
Region
                                                                                                     New DNA molecules, useful for producing ligands (which are useful regulating immune response and in screening for inhibitors of NF-creeptor activator) of the receptor activator of NF-chi B (RANK)
                                                                                                                                                   N-PSDB;
                                                                                                                                                                                  Anderson
                                                                                                                                                                                                                                                                                                                                                                                                chromosome
                                                                                                                                                                                                                                                                                                                                                                                                         Murine; receptor activator of NF-chi B; RANK; tumour necrosis factor; CD40; TNF receptor-associated factor; TRAF; ligand; immune response;
                                                                                                                                                                                                                                                                    22-DEC-1997;
                                                                                                                                                                                                                                                                                                             US6242213-B1
                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
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DB; AAD08714.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pammegswldvaqrgkpeaqpfahltinaasipsgshkvtlsswyhdrgwakisnmtlsn
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97US-0077181.
97US-0064671.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        activator
                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers 139..294
                                                                                                                                                                                                                                                                                                                                /note="Receptor binding region"
                                                                                    59-62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein;
                                                                                                                                                                                                                                                                                                                                                                                              RANKL; chromosome
                                                                                    43pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                        of NF-chi
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The present invention relates to a novel receptor, referred to as R (receptor activator of NF (nuclear factor)-kappaB), a member of TNF (tumour necrosis factor) receptor superfamily. RANK is a Type I
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30-MAR-1998; 16-APR-1997; 23-JUN-1997;

98US-0052521. 97US-0842842. 97US-0880855.

(AMGE-)

INC

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RESULT
AAE01992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                       Mouse; receptor activator of NF-kappaB; RANK; nuclear factor-kappaB; NF-kappaB; tumour necrosis factor; TNF; type I transmembrane protein; TNF receptor associated factor; TRAF; RANK ligand; RANKL; osteopathic;
                                                          New DNA encoding a receptor activator of NF-kappaB polypeptide treatment of Paget's disease and Familial Expansile Osteolysis
                                                                                                                                                                                                                                                                          inflammatory reaction; bone resorption; gene therapy; immune system dysfunction; familial expansile osteolysis; early onset Paget's disease of bone; EP; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                         31-JUL-2001
                                      Disclosure; Page 74-75; 96pp; English
                                                                                                                                                                     17-NOV-1999;
                                                                                                                                                                                        14-NOV-2000; 2000WO-US31459.
                                                                                                                                                                                                                                  WO200136637-A1
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                                                                                                                                                (IMMV ) IMMUNEX CORP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ligands are useful for regulating immune response and in screening inhibitors of RANK. The present sequence is murine RANKL protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKVQDID 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DSTHCFYRILRLHENADLQDSTLESEDTLPDSCRRMKQAFQGAVQKELQHIVGPQRFSGA 120
                                                                                            2001-329222/34.
DB; AAD05903.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  294;
                                                                                                                           DM,
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                                                                                                                           Hughes
                                                                                                                                                                     99US-0442029
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                                                                                                                                                                                                                                                                                                                                                    activator of NF-kappaB ligand) protein
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                                                                                                                                                                                                                                                                                                  immunomodulator;
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                                                              for the (FEO) -
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RESULT
AAW83194
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Best Local
                                                                                                                                                                                         Human; osteoprotegerin binding protein; OPG binding protein; arthri osteoporosis; osteoclast maturation; bone disease; metastasis; ODAR hypercalcaemia; osteoclast differentiation and activation receptor; Paget's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                         11-FEB-1999
                                                                                                                                                                                                                                                                                                                                             AAW83194 standard; Protein; 316
                                                                                15-APR-1998;
                                                                                                                                      W09846751-A1
                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                              Human osteoprotegerin binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                         (first entry)
                                                                                 98WO-US07584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 1561; DB 22; 100.0%; Pred. No. 2.4e-140;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Osteoprotegrin (OG) in biological samples; to screen for specific binding agents (particularly agonists and antagonists including cintracellular proteins); to raise Ab (useful in immunoassays for detection of OPG binding protein) and to identify compounds that modulate binding of OPG binding protein to osteoclast differentiation and activation receptor (ODAR). The nucleic acid molecule encoding OPG binding protein can be used to detect OPG binding protein-encoding CS sequences, e.g. screening for related sequences, also to produce CC transgenic animal models, while complementary sequences are used for antisense regulation of OPG binding protein expression, Modulators of OPG binding protein, particularly soluble forms of OPG binding protein complementary sequences, a steeporosis, bone loss caused by arthritis or metastases, hypercalcaemia, Paget's CC disease, periodontal disease, osteoporosis, loosening of prostheses, optionally in combination with agents that promote bone growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                      Osteoclastogenesis inhibitory factor; OCIF; OCIF-binding molecule; OBM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is human osteoprotegerin (OPG) binding protein. Host cells transfected with vectors containing nucleic acid molecules encoding OPG binding protein are used to produce recombinant OPG binding protein is used in binding assays to determine osteoprotegrin (OG) in biological samples; to screen for specific osteoprotegrin (OG) in biological samples; to screen for specific
            osteoclast;
                                                      Osteoclastogenesis
                                                                                      10-FEB-1999
                                                                                                                                                AAW83017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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N-PSDB; AAV70284.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acid encoding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ocal Similarity
                                                                                                                                                                                                                      WSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKVQDID
                                                                                                                                                                                                                                                                                                                                              PAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHKVTLSSWYHDRGWAKISNMTLSN 180
                                                                                                                                                                                                                                                                                                                                                                                                                           DSTHCFYRILRLHENADLQDSTLESEDTLPDSCRRMKQAFQGAVQKELQHIVGPQRFSGA 120
                                                                                                                                                                                                                                                                                                                                                                                                           dsthcfyrilrlhenaglqdstlesedtlpdscrrmkqafqgavqkelqhivgpqrfsga 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      293;
                                                                                                                                                 standard;
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         bone absorption factor; bone disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bone diseases
                                                      inhibitory
                                                                                                                                                 Protein; 316
                                                                                   entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99.6%;
99.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                osteoprotegrin binding protein - useful for, seases by modulating osteoclast differentiation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1554;
Pred. No. 1
                                                        factor
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                                                   (OCIF)-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 316;
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           calcium
                                                    molecule (OBM).
           metabolism
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15-APR-1997;
09-JUN-1997;
12-AUG-1997;
21-AUG-1997;
                                                                                                                                                                                                                                                                                                                   The present sequence represents an osteoclastogenesis inhibitory factor (OCIF) binding molecule (OBM). The protein promotes and supports the separation and maturation of osteoclasts in the presence of bone absorption factors such as calcitriol or parathyroid hormone (PFH). OBM is isolated from stroma cells cultured in the presence of a bone absorption factor by separation and solubilisation of membrane proteins then affinity chromatography using OCIF. It exists in a full-sequence form and a solubilised form (sOBM) which is a shorter chain. OBM may be used for screening potential inhibitors and modifiers of its biological activity, and screening for receptors to OBM which mediate its function. These substances can then be used in the treatment of disorders of bone function and calcium metabolism. The antibodies can be used for assay of the protein, for investigative and diagnostic purposes, and as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein binding to osteoclastogenesis inhibitory factor - useful for, e.g. treatment and investigation of disorders of bone and
                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Goto M, Higashio K,
Nakagawa N, Shima N,
Washida N, Yamaguchi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        calcium
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    263
                         241
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\tt dsthcfyrilr lhen aglqdstlesedtlpdscrrmkqafqgavqkelqhlvgpqrfsga
                                                                                                                                                    DSTHCFYRILRLHENADLODSTLESEDTLPDSCRRMKQAFQGAVQKELQHIVGFQQRFSGA 120
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                                                                                                                                                                                                                                       293;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8; Pages 106-108;
                                                                                                                                                                                                                                                 Similarity
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97JP-0097808.
97JP-0151434.
97JP-0217897.
97JP-0224803.
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                                                                                                                                                                                                                                               99.6%;
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Takahashi K,
K, Yano K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            151pp; Japanese.
                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                               Score 1554;
Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tomoyasu
Yasuda H;
                                                                                                                                                                                                                                               DB 19;
1.2e-139;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW59654 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Amino acid sequence of mouse 499E9, protein
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                                                                                                                                                                                                                                                                                                                                                                                       This is the amino acid sequence of the mouse 499E9 protein, used in the method of the invention to treat conditions associated with abnormal physiology or development. The 499E9 protein is expressed highly on polarised Thi T cells, binding of 499E9 to its receptor may result in either immune cell expansion or apoptosis. Antagonists of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Pages 8-11; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse cell surface antigen, 499E9 protein - used to treat conditions associated with abnormal physiology or development
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1998-348452/30
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 83
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                              DSTHCFYRILRLHENADLQDSTLESEDTLPDSCRRMKQAFQGAVQKELQHIVGPQRFSGA 120
                                                     GVPHEGPLHPAPSAPAPAPAPAPAPARASRSMFLALLGLGLGQVVCSIALFLYFRAQMDPNRISE 60
Similarity
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lupus erythematosus; Hashimoto's autoimmune thyroiditis;
flammatory response; antibody; antigen; cancer.
                                                                                                                                                                                               316 AA;
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                                                                                                                    Conservative
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                                                                                                                                    99.6%;
99.7%;
                                                                                                                    Score 1554; DB 19; pred. No. 1.2e-139; 0; Mismatches 1;
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                                                                                                                        Indels
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                    The present sequence represents murine TNF-related activation induced CC cytokines (TRANCE). Human or murine TRANCE polypeptides or their CC variants, fragments, derivatives or analogues may be used as modulators of immune response in a mammal comprising, antisense sequences to CC of immune response in a mammal comprising, antisense sequences to CC RANCE and fusion proteins comprising human and/or murine TRANCE.

CC Agonists and antagonists of TRANCE, can be used to modulate immune creasing or decreasing the life span of mature dendritic CC cells and increasing or decreasing T cell activation. These techniques are especially useful for treating immune system related conditions such CC as HIV, cancer, autoimmune disease or hypersensitivity to an allergen. The TRANCE polypeptides can be used to increase the viability of CM centric cells in vivo or in vitro, especially when used in conjunction with proteins of the tumour necrosis factor (TNF) superfamily (especially CD40L or TNF-alpha).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANCE; tumour necrosis factor superfamily; signal transduction; TNF-related activation induced cytokine; immune response; cancer autoimmune disease; HIV; hypersensitivity; allergen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Murine TRANCE
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                                                                                                                                                                                                                                                                                                              Choi Y,
                                                                                                                                                                                                                                                                                                                                                              03-MAR-1998;
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12-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                 14-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
Sequence
                                                                                                                                                                                                                     Claim 9; Fig 3; 164pp; English
                                                                                                                                                                                                                                              TNF like proteins for treating autoimmunity and cancer
                                                                                                                                                                                                                                                                                    WPI; 1999-385609/32
                                                                                                                                                                                                                                                                                                                                   (UYRQ ) UNIV ROCKEFELLER
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97US-0989479.
98US-0034099.
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Query Match
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Matches 293; Conserv

Conservative

99.6%; 99.7%;

Score 1554; DB zv; Pred. No. 1.2e-139;

Length Indels

316; 0;

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                             The present invention describes a genomic DNA encoding a protein having an activity of supporting or promoting differentiation and maturation of osteoclasts. The genomic DNA encoding a protein has the following properties: (a) combines specifically with osteoclastogenesis inhibitory factor (OCIF) and has a high affinity; (b) shows a molecular weight (mw) of 30,000 to 40,000 by SDS-PAGE (sodium dodecyl sulfate-polyacrylamide gel electrophoresis) under a nonreductive condition and the apparent mw when crosslinked with monomer type OCIF is 90,000 to 10,000; and (c) has an activity of supporting or promoting differentiation and maturation of osteoclast in the co-culture of mouse osteoblast-like stroma cell and mouse spleen cell in the presence of a bone absorption promoting factor such as active type vitamin D3 and parathyroid hormone (PTH). The protein represents a mouse OCIF binding molecule (OBM) from the present
                                                                                                                                                                                                                                                                                                            (YSNE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse; osteoclastogenesis inhibitory factor binding molecule; OCIF; OBM; osteoclast; bone absorption promoting factor; vitamin D3; PTH; parathyroid hormone.
                                                                                                                                                                                                                                            A DNA and preparation of a protein by using
                                                                                                                                                                                                                     Example 1; Page 15-16; 18pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                30-SEP-1998;
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DB; AAA39156.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OBM protein sequence
                                                                                                                                                                                                                                                                                                           YS NEW TECHNOLOGY KENKYUSHO.
                                                                                                                                                                                                                                                                                                                                                98JP-0292971.
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Sequence

316 AA

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RESULT 1
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Matches 293
                 In vivo do to treat,
                                                                                                                                                                                                                                                                                       Osteoprotegerin ligand; OPGL; osteoprotegerin; osteoclastogenesis; tumour necrosis factor receptor; type II transmembrane protein; osteoclast differentiation; CSF-1; osteoclast activator; immune response; osteoporosis; bone resorption.
                                                                                                      15-SEP-1998;
02-OCT-1998;
  Claim
                                                     WPI;
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                                                                                                                                                                                            Region
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                                                                                                                                                                                                                              Domain
                                                                                                                                                                                                                                                                        Mus musculus
                                                                                                                                                                                                                                                                                                                                   Amino acid
                                                                                      (MEBI-) M & E
                                                                                                                                                                 WO200015807-A1
                                                                                                                                                                                                                                               Domain
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                                                                                                                                                                                                                                                                                                                                                                                      AAY84418 standard; Protein;
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thes 293;
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                                                                                                                                                                                                                                                                                                                                                                                                                              GKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVYVVKTSIKIPSSHNLMKGGSTKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GVPHEGPLHPAPSAPAPAPAPPPAASRSMFLALLGLGLGQVVCSIALFLYFRAQMDPNRISE
                                                                                                                                                                                                                                                                                                                                                                                                                                                               gklrvnqdgfyylyanicfrhhetsgsvptdylqlmvyvvktsikipsshnlmkggstkn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    {\tt gvphegplhpapsapapapapasrsmflallglggqvvcsialflyfraqmdpnrise}
  17;
                          down-regulation of osteoprotegerin ligand
                                            AAZ99965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
  Page
                   prevent and ameliorate osteoporosis
                                                                                                                                                                                                                                                                                                                                sequence of a murine osteoprotegerin ligand (OPGL).
                                                                     Haaning
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                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                      BIOTECH AS
  81-82;
                                                                                                      98DK-0001164
98US-0102896
                                                                                                                                99WO-DK00481
                                                                                                                                                                                                                             /note=
70..157
                                                                                                                                                                                                                                              Location/Qualifiers 48..71
                                                                                                                                                                                           /note-
158..31
                                                                                                                                                                                                            /note= "extracellular stalk domain'
152..316
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110pp;
                                                                                                                                                                                                                                      "transmembrane
                                                                                                                                                                                  "active
                                                                                                                                                                                                  "tumour necrosis factor-like
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Pred. No. 1.2e-139;
0; Mismatches 1;
                                                                                                                                                                                 ligand moiety"
                                                                                                                                                                                                                                      domain"
                          (OPGL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
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                                                                                                                                                                                                  domain"
                          activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        316;
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RESULT 1
AAY84419
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Best Local Similarity
Matches 293; Conserv
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                                                                                                                                                                                                                                                                  Osteoprotegerin ligand; OPGL; osteoprotegerin; osteoclastogenesis; tumour necrosis factor receptor; type II transmembrane protein; osteoclast differentiation; CSF-1; osteoclast activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY84419
                                                                                             Region
                                                                                                                                                                                  Key
                                                                                                                                                                                                                  Mus musculus
                                                                                                                                                                                                                                                                                                                                     Amino acid sequence of a murine osteoprotegerin ligand (OPGL).
              23-MAR-2000
                                               WO200015807-A1
                                                                                                                                 Domain
                                                                                                                                                                 Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKVQDID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gklrvnqdgfyylyanicfrhhetsgsvptdylqlmvyvvktsikipsshnlmkggstkn
                                                                                                                                                                                                                                                     response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or
                                                                                                                                                                                                                                                                                                                                                                                                                                          standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      316 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    conditions characterised by excessive bone resorption.
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                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                 /note= '70..157
                                                                             /note= "extracellular stalk domain" 158..317 /note= "active ligand moio+v"
                                                                                                                                                                 Location/Qualifiers 49..69
                                                                                                                                                                                                                                                     osteoporosis; bone
                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99.6%;
99.7%;
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Pred. No. 1.2e-139;
0; Mismatches 1;
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      manner. The OPGL protein is synthesised as a type II transmembrane protein. The murine and human OPGL polypeptides are 87% homologous. OPGL is a potent osteoclast differentiation factor when combined with CSF-1. It is not capable of inducing osteoclast differentiation in the absence of CSF-1. OPGL is also an activator of mature osteoclasts. The specification describes a method for the in vivo down-regulation of OPGL activity in an animal. The method comprises using at least one OPGL polypeptide or subsequence, and/or at least one OPGL analogue to induce an immune response in the animal. The method and OPGL polypeptide are useful for treating, preventing and amellorating osteoporosis or other diseases or conditions characterised by excessive bone resorption.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents a murine osteoprotegerin ligand (OPGI osteoprotegerin is a secreted member of the tumour necrosis factor receptor family, which blocks osteoclastogenesis in a dose dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 17; Page 85-86; 110pp;
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                                                                                                                              AAB82092 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
         Osteoclast Differentiation
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                                                                                                                                                                                                                                                                                                                                                                                                          osteoclast
                                                                                                                                                                                                                                                2000-271444/23
                                                                                                                                                                                                                                                                                                                              PAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHKVTLSSWYHDRGWAKISNMTLSN 180
                                                                                                                                                                                                                                                                                                                                                                       DSTHCFYRILRLHENADLQDSTLESEDTLPDSCRRMKQAFQGAVQKELQHIVGPQRESGA 120
                                                                                                                                                                                             WSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKVQDID
                                                                                                                                                                                                                                                                                                     {\tt pammegswldvaqrgkpeaqpfahltinaasipsgshkvtlsswyhdrgwakisnmtlsn}
                    osteoclast formation inducer; vaccine; gene therapy;
                                                                                                                                                                                                                                                                                                                                                          dsthcfyrilrlhenaglqdstlesedtlpdscrrmkqafqgavqkelqhivgpqrfsga
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                                                                            (first entry)
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98US-0102896
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                                                   differentiation factor, ODF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99.6%;
99.7%;
             Factor;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1554;
Pred. No. 1
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               bone
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1.2e-139;
hes 1;
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RESULT 1
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel nucleic acid encoding rat osteoclast differentiation useful for modulating activity of a cell, e.g., cell prolif
                              Human osteoprotegerin binding protein from the pcDNA/huOPGbp1.linsert.
                                                                                                                    AAW83195 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 5; Fig 2; 8lpp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cell differentiation and cell viability
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                                                                                                                                                                                                                                                sngklrvnqdgfyylyanicfrhhetsgsvpadylqlmvyvvktsikipsshnlmkggst
                                                                                                                                                                                                                                                                 SNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVYVVKTSIKIPSSHNLMKGGST 238
                                                                                                                                                                                                                                                                                                                         GAPAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHKVTLSSWYHDRGWAKISNWTL 178
                                                                                                                                                                                                                                                                                                                                                                                  DSTHCFYRILRLHENADLQDSTLESEDT--LPDSCRRMKQAFQGAVQKELQHIVGPQRFS 118
                                                                                                                                                                                                                        KNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKVQDID
                                                                                                                                                                                                                                                                                                           gvpammegswldvarrgkpeagpfahltinaadipsgshkvslsswyhdrgwakisnmtl
                                                                                                                                                                                                                                                                                                                                                                                                                        gvphegplhpapsapapappaasrfmflallglglgqvvcsialflyfragmdpnrise 82
                                                                                                                                                                                                                                                                                                                                                                 dstrcfyrilrlrentglqdstlesedtealpdscrrmkqafqgavqrelqhivgpqrfs 142
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osteoprotegerin binding protein; OPG binding protein; arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zheng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                     Protein;
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Pred. No. 1e-133;
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DSTHCFYRILRLHENADLQDSTLESEDT--LPDSCRRMKQAFQGAVQKELQHIVGPQRFS

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KNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKVQDID 294 sngklivnqdgfyylyanicfrhhetsgdlateylqlmvyvtktsikipsshtlmkggst SNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVYVVKTSIKIPSSHNLMKGGST aekamvdgswldlakrskleaqpfahltinatdipsgshkvslsswyhdrgwakisnmtf 201 GAPAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHKVTLSSWYHDRGWAKISNMTL 178 dgthciyrilrlhenadfqdttlesqdtklipdscrrikgafqgavqkelqhivgsqhir 141

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The present sequence is human osteoprotegerin (OPG) binding protein.
CC Host cells transfected with vectors containing nucleic acid molecules
CC encoding OPG binding protein are used to produce recombinant OPG binding
CC protein. OPG binding protein is used in binding assays to determine
CC protein. OPG binding protein is used in binding assays to determine
CC binding agents (Particularly agonists and antagonists, including
CC intracellular proteins); to raise Ab (useful in immunoassays for
CC detection of OPG binding protein) and to identify compounds that
CC modulate binding of OPG binding protein to osteoclast differentiation
CC and activation receptor (ODAR). The nucleic acid molecule encoding OPG
CC binding protein can be used to detect OPG binding protein-encoding
CC sequences, e.g. screening for related sequences, also to produce
CC transgenic animal models, while complementary sequences are used for
CC of antisense regulation of OPG binding protein expression. Modulators of
CC or Ab, are used to treat or prevent bone diseases, e.g. osteoporosis,
CC one loss caused by arthritis or metastases, hypercalcaemia, Paget's
CC disease, periodontal disease, osteoporosis, loosening of prostheses,
CC optionally in combination with agents that promote bone growth.
   Query Match
Best Local Sin
Matches 250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB;
                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 19; Fig 4; 47pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid encoding osteoprotegrin binding protein - useful for, e.g. treating bone diseases by modulating osteoclast differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1998-594578/50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Boyle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAR-1998;
16-APR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            osteoporosis; osteoclast maturation; bone disease; metastasis; ODAR; hypercalcaemia; osteoclast differentiation and activation receptor; Paget's disease.
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                      Similarity
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97US-0842842.
97US-0880855.
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                    85.0%;
Score 1326.5; DB 15;
Pred. No. 5.7e-118;
Pred. No. 5.7e-218;
                                      DB 19; Length 317;
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262 kywsgnsefhfysinvggffklrsgeelsievsnpslldpdqdatyfgafkvrdid

317

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RESULT 15
AAW69957
                  Query Match
Best Local Similarity
 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-OCT-1997;
23-DEC-1996;
07-MAR-1997;
                                                                                                                                       allo-stimulatory capacity, thereby augmenting an immune response. The soluble RANK polypeptide composition may also be used for regulating an immune or inflammatory response. Inhibition of NF-kB by RANK antagonists may be useful in ameliorating negative effects of an inflammatory response that result from triggering of RANK, e.g. in treating toxic shock or sepsis, graft-versus-host reactions, or acute inflammatory reactions. They can also be used in adjunct therapy for disease characterised by neoplastic cells that express RANK. RANKL polypeptides can also be used to identify inhibitors of RANK and thus inhibitors of an inflammatory response, and also for protecting RANK-expressing cells from the negative effects of chemotherapy or the presence of high levels of TNF-alpha. The products can also be used for detection and drug
                                                                                                                                                                                                                                                                                                                                                      This represents a human RANKL, a ligand for the RANK (receptor activator of necrosis factor-kappaB (NF-kB)) polypeptide. RANK is a member of the tumour necrosis factor (TNF) family. A soluble RANK may be used for inhibiting activation of NF-kB, by contacting a cell expressing membrane-associated RANK with a soluble RANK which binds to RANK ligand (RANKL). RANKL polypeptides can activate RANK and can be used to induce maturation of dendritic cells and enhance their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1998-377657/32.
N-PSDB; AAV41378.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RANK; necrosis factor-kappa B; NF-kB; receptor activator; human; immune response; inflammatory response; toxic shock; sepsis; RANKL; RANK ligand; tumour necrosis factor; TNF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 27; Pages 59-60; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated ligand for receptor activator of NF-kappa B ^{\rm -} used to develop products for augmenting an immune response for inhibiting an inflammatory response and for protection of cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW69957 standard; Protein;
                                                                                         Sequence
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   Conservative
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96US-0059978.
97US-0813509.
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                  85.0%;
84.5%;
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                  Score 1326.5; DB 19; Length Pred. No. 5.7e-118;
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                                                                                KNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKVQDID
kyws gnsefh fy sinv ggffklrs gee is {\tt ievsnpslldpdqdatyfgafkvrdid}
                                         \verb|sngklivnqdgfyylyanicfrhhetsgdlateylqlmvyvtktsikipsshtlmkggst|\\
                                                   SNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVYVVKTSIKIPSSHNLMKGGST
                                                                                                                                                                 {\tt gaphegplh-appppaphqppaasrsmfvallglglgqvvcsvalffyfraqmdpnrise}
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Search completed: Job time: 698 sec July 8 2002, 20:05:54

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Sequence 33, Appli
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Perfect score:
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         US-09-865-363-11
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1 GVPHEGPLHPAPSAP
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         GenCore version 4.5 (c) 1993 - 2000 Comp
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US-08-915-649A-11
US-08-989-362-2
US-08-996-139-13
US-08-995-6139-13
US-08-995-629-13
US-08-995-6321C-4
US-09-052-521C-4
US-09-052-521C-4
US-09-072-993C-3
US-08-670-354-2
US-08-684-031-1
US-08-684-031-1
US-08-684-031-1
US-08-684-031-1
US-09-320-424-6
PCT-US96-10895-2
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US-09-320-424-11
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                  US-08-996-139-11
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US-08-996-139-11
                                                                                                                       CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 60/064,671

FILING DATE: 14 OCTOBER 1997

PRIOR APPLICATION DATA:

APPLICATION UMBER: USSN 08/813,509

FILING DATE: 07 MARCH 1997

PRIOR APPLICATION DATA:

APPLICATION DATA:

APPLICATION UMBER: USSN 08/772,330

FILING DATE: 23 DECEMBER 1996

ATTORNEY/AGENT INFORMATION:

NAME: PETKINS, PATTICIA Anne
REGISTRATION NUMBER: 33,693

REFERENCE/DOCKET NUMBER: 2851-A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206)587-0430
                                           TELEPHONE: (206)587-043
TELEPAX: (206)233-0644
INFORMATION FOR SEO ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 294 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 11,
Patent No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 51
CITY: Seattle
STATE: WA
CCOUNTRY: USA
TIP: 98101
TIP: 710ADABI
                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operati
                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Microsoft WC CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 22 DEC
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6017729
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51 University Street
                                                                        294 amino acids
                                                                                                  (206)233-0644
(206)277 TO NO: 11:
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22 DECEMBER 1997
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                                                                                                                                                                                                                                                                                                                                                                                                           Word for Power
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US-08-339-214-32
US-08-815-190A-2
US-08-815-190A-2
US-09-290-640-25
US-09-290-640-25
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US-08-484-6248-12
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Result

Minimum Maximum

Searched:

Database

Length 294; Indels

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Gaps

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RESULT 2
US-08-995-659-11
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                 TELEFAX: (206)233-064
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Galibert, Laurent
APPLICANT: MarasKovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: Apple Power MacIntosh
OPERATING SYSTEM: Apple Operating System 7.5.
SOFTWARE: Microsoft Word for Power MacIntosh
CURRENT APPLICATION DATA:
                                                              REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                               FILING DATE: 07 MARCICLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Anderson, Dirk M.
                                                                                                                                           CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 5.
STREET: 5.
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                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: 14 OC
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/995,659 FILING DATE: 22 DECEMBER 1997
                                                                                                                                                                                                                                                       APPLICATION NUMBER: US FILING DATE: 07 MARCH
                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION
                                                   TELEPHONE:
                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
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CHARACTERISTICS:
                                                                                                                        Perkins, Patricia Anne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51 University Street
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                                  (206)233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunex Corporation, Law Department
                                                   (206)587-0430
                                                                                                                                                                               23 DECEMBER
                                                                                                                                                                                                                                                                                                                            14 OCTOBER 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 1561; DB 3; 100.0%; Pred. No. 2.8e-153;
                                                                                                                                                                                                                                                                                                                                               USSN 60/064,671
                                                                                                                                                                               USSN 08/772,330
EMBER 1996
                                                                                                                                                                                                                                                                         USSN 08/813,509
                                                                                                                                                                                                                                                       1997
                 11:
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US-09-215-649A-11
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Best Local Similarity
Matches 294; Conserv
     INFORMATION FOR
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OPERATING SYSTEM: Apple Operating System 7.5.
SOFTWARE: Microsoft Word for Power Macintosh
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/215,649A
FILING DATE: 17-Dec-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:

OPERIOR APPLICATION DATA:
                                      TELECOMMUNICATION INFORMATION: TELEPHONE: (206)587-0430
                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851
                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Receptor Activator of NF-kappaB NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Anderson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKVQDID 294
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   TELEFAX: (
                                                                                                                                             APPLICATION NUMBER: 08/996,139
FILING DATE: <UNKNOWN>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
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Pred. No. 2.8e-153;
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; MOLECULE TYPE: protein US-08-842-842-7
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US-08-842-842-7
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Ver

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/842,842

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Winter Robert B.

REFERENCE/DOCKET NUMBER: A-451

INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-215-649A-11
 Query Match
Best Local Similarity
Matches 293; Conserv
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Best Local Similarity 100.0%;
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APPLICANT: BOYLE, WILLIAM
TITLE OF INVENTION: OSTEOF
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 316 amino acids
TYPE: amino acid
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CITY: Thousand Oaks
STATE: California
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SEQUENCE DESCRIPTION: SEQ ID
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LENGTH: 294 amino acids
TYPE: amino acid
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1840 Dehavilland Drive
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   Conservative
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              Score 1554;
Pred. No. 1.
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Pred. No. 2.8e-153;
   Mismatches
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              ; DB 2;
1.7e-152;
                              Length 316;
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; MOLECULE TYPE: US-08-989-362-2
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US-08-989-362-2
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                                                                                                                 TELEFAX: (650)496-1204
INFORMATION FOR SED ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 316 amino acids
TYPE: amino acid
TOPOLOGY: linear
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 Matches
                    Query Match
Best Local
                                                                                                                                                                                                               CLASSIFICATION: 56
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/032
PILING DATE: 13-DCC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX06
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650,852-9196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/989,362 FILING DATE: 12-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Gorman, Daniel M.
APPLICANT: Mattson, Jeanine D.
TITLE OF INVENTION: Mammalian Cell Surface Antigens; Related
TITLE OF INVENTION: Reagents
NUMBER OF SEQUENCES: 2
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                 Local
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   l Similarity
293; Conserv
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   Conservative
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                 99.6%;
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Score 1554; DB 4;
Pred. No. 1.7e-152;
0; Mismatches 1;
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                               Length 316;
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US-09-052-521C-2
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        US-08-996-139-13
Sequence 13, Application US/08996139
Patent No. 6017729
GENERAL INFORMATION:
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; LENGTH: 316
; TYPE: PRT
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                          Matches
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PRIOR FILING DATE: 1997-06-23
PRIOR APPLICATION NUMBER: 08/2
PRIOR FILING DATE: 1997-04-16
NUMBER OF SEQ ID NOS: 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Boyle, William J.
TITLE OF INVENTION: OSTEOPRO-
FILE REFERENCE: A-451Brv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/052,521C CURRENT FILING DATE: 1998-03-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Mouse
APPLICANT:
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                                                                                                                                           293;
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Anderson,
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99.7%;
Dirk M.
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              US-08-995-659-13
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Best Local S
Matches 250
Sequence 13,
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US/08/996 122
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FILING DATE: 14 OCTOBER 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
DETCE APPLICATION TO MARCH 1997
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APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Receptor Activator NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
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                                                                                                                                                                                                  COMPUTER: Apple Power Macintosh OPERATING SYSTEM: Apple Operating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 51 Un:
CITY: Seattle
                                                                              262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid TOPOLOGY: linear
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nes 250; Conserva
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                                                                                             KNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLLDPDQDATYFGAFKVQDID 294
                                                                                                                                      SNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVYVVKTSIKIPSSHNLMKGGST 238
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 Application US/08995659
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                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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84.5%;
                                                                                                                                                                                                                                                                                                                                                                                               16;
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; Pred. No. 5.4e.
16; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                 4e-129;
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US-08-995-659-13
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Best Local Similarity
Matches 250; Conserv
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INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 317 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laucent
APPLICANT: Galibert, Laucent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
239 KNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKVQDID 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power MacIntosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power MacIntosh 6.
CURRENT APPLICATION DATA:
                                                                                 179 SNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMYYVVKTSIKIPSSHNLMKGGST 238
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FILING DATE: 22 DECEMBER 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/064,671
FILING DATE: 14 OCTOBER 1997
                                                         202 SNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMVYVTKTSIKIPSSHTLMKGGST
                                                                                                                                        142 AEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSHKVSLSSWYHDRGWAKISNMTF 201
                                                                                                                                                                119 GAPAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHKVTLSSWYHDRGWAKISNMTL 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Perkins, Patricia Anne REGISTRATION NUMBER: 34,693 REFERENCE/DOCKET NUMBER: 2852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
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23 DECEMBER 1996
                                                                                                                                                                                                                                                                                                                                                                                   85.0%; Score 1326.5; DB 4; Length 317; 84.5%; Pred. No. 5.4e-129; ative 16; Mismatches 27; Indels 3;
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                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 13:
179 SNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVYVVKTSIKIPSSHNLMKGGST 238
                                                                                                         119 GAPAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHKVTLSSWYHDRGWAKISNWTL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 08/996,139
FILING DATE: CUNKNOWN>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
                                                                                                                                                                               82
                                                                                                                                                                                       61 DSTHCFYRILRLHENADLQDSTLESEDT--LPDSCRRMKQAFQGAVQKELQHTVGPQRFS 118
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                                                                                                                                                                                                                                                     23 GAPHEGPLH-APPPPAPHQPPAASRSMEVALLGLGLGQVVCSVALFFYFRAQMDPNRISE
                                                                                                                                                                                                                                                                                        1 GVPHEGPLHPAPSAPAPAPPPAASRSMFLALLGLGLGQVVCSIALFLYFRAQMDPNRISE
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.
SOFTWARE: Microsoft Word for Power Macintosh
CURRENT APPLICATION DATA:
                                                                              AEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSHKVSLSSWYHDRGWAKISNMTF 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
                                                                                                                                                               DGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIKQAFQGAVQKELQHIVGSQHIR 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 98101
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: RECEPTOR ACTIVATOR OF NF-kappaB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Anderson, Dirk M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/215,649A FILING DATE: 17-Dec-1998 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 317 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: WA
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                                                                                                                                                                                                                                                                                                                                   85.0%; Score 1326.5; DB 4;
84.5%; Pred. No. 5.4e-129;
.4.5%; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Law Department
                                                                                                                                                                                                                                                                                                                                                                           DB 4; Length 317;
                                                                                                                                                                                                                                                                                                                                      Indels
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US-09-052-521C-4
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US-09-052-521C-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-072-993C-3
                                    CURRENT FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/055,513
PRIOR FILING DATE: 1997-08-13
PRIOR APPLICATION NUMBER: 60/056,980
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/057,550
PRIOR FILING DATE: 1997-08-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Boyle, William J.
TITLE OF INVENTION: Osteoprotegerin Binding Proteins
FILE REFERENCE: A 451BrV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/09052521C Patent No. 6316408
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                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Michael R. Brigham-Burke
APPLICANT: Peter R. Young
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Best Local Similarity
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PRIOR APPLICATION NUMBER: 08/6
PRIOR FILING DATE: 1997-04-16
NUMBER OF SEQ ID NOS: 40
SOFTWARDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/052,521C CURRENT FILING DATE: 1998-03-30 PRIOR APPLICATION NUMBER: 08/880,855 PRIOR FILING DATE: 1997-06-23
                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/09072993C Patent No. 6346388
                                                                                                                                                                                                                                               TITLE OF INVENTION: A METHOD OF IDENTIFYING AGONIST TITLE OF INVENTION: ANTAGONISTS FOR THACK THE DESCRIPTION AND 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE:
                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/072,993C CURRENT FILING DATE: 1998-05-06
                                                                                                                                                                                                                                             FILE REFERENCE: GH-50030
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAPAMMEGSWILDVAQRGKPEAQDFAHLTINAASIPSGSHKVTLSSWYHDRGWAKISNMTL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVYVVKTSIKIPSSHNLMKGGST 238
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                       SEQ ID NOS:
FastSEQ
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for Windows Version
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84.5%;
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Pred. No. 5.4e-129;
Pred. No. 5.4e-129;
Pred. No. 5.4e-129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4;
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US-08-670-354-2
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; LENGTH: 279
; TYPE: PRT
; ORGANISM: HOMO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 16.6
Best Local Similarity 26.4
Matches 78; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Microsoft Word, Vers CURRENT APPLICATION DATA:
APPLICATION NUMBERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Steven R. Wiley and APPLICANT: Raymond G. Goodwin. TITLE OF INVENTION: Cytokine That Induces
                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/496,632
FILING DATE: 29-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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                                                                                                                                                                               APPLICATION NUMBER: US 01 FILING DATE: 01-NOV-1995 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     223 SARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 235 GGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNFSLLDPDQDATYFGAFKV 290
                                                             REGISTRATION NUMBER: 32,172
REFERCE/DOCKET NUMBER: 32
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk COMPUTER: Apple Macintosh OPERATING SYSTEM: Apple 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP:
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                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Kathryn A. Anderson, STREET: 51 University Street
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                                                           TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EGSWLDVAORGKPEAQPFAHLT----INAASIPSGSHKVTL----SSWYHDR-GWAKIS 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WDP--NDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPL-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGTACF-----LKEDDSY 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98101
                                                                                                                                                               Anderson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WΑ
                                      (206) 233-0644
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                                                                                                                                Kathryn A.
BER: 32,172
                                                                                                                                                                                                                                                               US 08/548,368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Word, Version
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; Pred. No. 1.1e-18;
54; Mismatches 113;
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Sequence 1, Application US/08584031A
Patent No. 6030945
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: APO-2 LIGAND
FILE REFERENCE: 11669.22US03
CURRENT APPLICATION NUMBER: US/08/584,031A
CURRENT FILING DATE: 1996-01-09
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 281
TYPE: PAT
ORGANISM: Homo saplens
US-08-584-031-1
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US-08-584-031-1
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Best Local S
Matches 78
                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local :
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SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: amino acid
TYPE: bmino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
        166
                                   175 NMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVYVVKTSIKIPSSHNLMK 234
                                                                                                             125 EGSWLDVAQRGKPEAQPFAHLT----INAASIPSGSHKVTL----SSWYHDR-GWAKIS 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               114
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                                                                                                                                                     65 WDP--NDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPL------
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                                                                                                                                                                                                                                  10 PSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACF----LKEDDSY 64
                                                                                                                                                                                                                                                                       21 PAASRSMFLALLGLGLGQVVCSIALFLYFRAQMD--PNRISEDSTHCFYRILRLHENADL 78
                                                                                                                                                                                                                                                                                                                   Local Similarity 26.4
nes 78; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16.6%; Score 258.5; DB 1; Local Similarity 26.4%; Pred. No. 1.1e-18; nes 78; Conservative 54.
                                                                                                                                                                                            QDSTLESEDTLPDSCRRMKQAFQGAVQK------ELQHIVGPQRFSGAPAMM 124
NLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYT-SYPDPILLMK 224
                                                                          ----VRERGPQRVA--AHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----VRERGPQRVA--AHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLS 165
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                                                                                                                                                                                                                                                                                                                 16.6%; Score 258.5; DB 3; Length 26.4%; Pred. No. 1.1e-18; ative 54; Mismatches 113; Indels
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US-08-883-086-10
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US-08-780-496-1
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NAME: MAISCHANG, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P0971
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/952-9881
TELEPAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: Amino acids
TYPE: Amino acids
TYPE: Amino acids
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Sequence 10,
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Best Local S
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MEDIUM TYPE: 3.5 inch, 1.44 mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
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CURRENT APPLICATION DATA:
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TITLE OF INVENTION: Apo-2 Ligand
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                       225
                                                                                                                                                                                                                                                           114 -----VRERGPQRVA--AHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLS 165
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                                                                                                SARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV
                                                                                                                                     GGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKV 290
                                                                                                                                                                              NLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYT-SYPDPILLMK
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                                                                                                                                                                                                                                                                                                                                                                                                                        PSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACF----LKEDDSY 64
                                                                                                                                                                                                                                                                                                    EGSWLDVAQRGKPEAQPFAHLT-----INAASIPSGSHKVTL----SSWYHDR-GWAKIS 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16.6%; Score 258.5; DB 3;
26.4%; Pred. No. 1.1e-18;
Vative 54; Mismatches 113;
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Application US/08883086

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; TOPOLOGY: linear; MOLECULE TYPE: No. 6171787e US-08-883-086-10
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INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 16.6%; Score 258.5; DB 4; Best Local Similarity 26.4%; Pred. No. 1.1e-18; Matches 78; Conservative 54; Mismatches 113;
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APPLICANT: WILEY, STEVEN
TITLE OF INVENTION: MEMBER OF THE THE FAMILY USEFUL
TITLE OF INVENTION: FOR TREATMENT AND DIAGNOSIS OF DISEASE
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSE: A
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ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
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SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: 847-937-0378
                                                                                                                                                           166
                                                                                                                                                                                               114 -----VRERGPORVA--AHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLS 165
                                                                                                                                                                                                                                                                                                                                                               125 EGSWLDVAQRGKPEAQPFAHLT-----INAASIPSGSHKVTL-----SSWYHDR-GWAKIS 174
225 SARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 280
                                            235 GGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKV 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: POTEMBSKI, Priscilla E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 6134.US.01
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STATE: IL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 PSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACF-----LKEDDSY 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QDSTLESEDTLPDSCRRMKQAFQGAVQK------ELQHIVGPQRFSGAPAMM 124
                                                                                                                                                           E: Abbott Laboratories
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Search completed: July Job time: 4195 sec

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Result
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Maximum DB
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Perfect score:
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ALIGNMENTS

RESULT 2 A49266 fas ligand - rat C;Species: Rattus norvegicus (Norway rat) C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change C;Accession: A49266 R;Suda, T; Takahashi, T.; Golstein, P.; Nagata, S. Cell 75, 1169-1178, 1993 A;Title: Molecular cloning and expression of the Fas ligand, a n A;Reference number: A49266; MUID: 94084792 CD40 ligand - bovine C;Species: Bos primigenius taurus (cattle) C;Species: Bos primigenius taurus (cattle) C;Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #; C;Accession: S53090 R;Mertens, B.E.L.C.; Muriuki, M. submitted to the EMBL Data Library, February 1995 A;Description: Cloning of bovine CD40L and homology A;Reference number: S53090 A; Molecule type: mRNA A; Residues: 1-261 <MER> A; Reference number: A; Accession: \$53090 A; Cross-references: A; Status: preliminary Query Match Best Local S Matches 71 214 243 164 113 186 129 65 69 10 PAPSAPAPAPAPASRSMELALLGIGIGQVVCSIALF-LYFRAQMDPNRISEDSTHCFYR Local Similarity mes 71; Conserv œ SKPCGQQSIHLGGVFELQSGASVFVNVTDPSQVSHGTGFTSFGLLKL GNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKV NQDGFYYLYANICF-RHHETSGSVPTDYLQLMVYVVKTSIKIPSSHN--LMKGGSTKNWS ---MHKGDQEPQIAAHV-----ISEASSKTTSVLQWAPKGYYTLSNNLVTLENGKQLAV FMKTIQRCNKGEGSLSLL-----NCEEIRSRFEDLVKDIMQN----KEVKKKEKNFE---KRQGFYYIYTQVTFCSNRETLSQAP-----FIASLCLKSPSGSERILLRAANTH--S LDVAQRGKPEAQPFAHLTINAASIPSGSHKVTLSSWYHDRGWAKISN--MTLSNGK-LRV 185 ILRLHENADLQDSTLESEDTLPDSCRRMKQAFQGAVQKELQHIVGPQRFSGAPAMMEGSW 128 PSPRSVATGPP--VSMKIFMYLLTVFLITQMIGSALFAVYLHRRLDKIE-DERNLHEDFV Conservative EMBL: 248469; NID: g732569; PIDN: CAA88363.1; PID: g732570 11.9%; 54; Score 185.5; DB 2 Pred. No. 2.9e-08; Mismatches 122; Indels 2 #text_change ៩ Length bovine 261 261; TNFA 41; 05-Nov-1999 Gaps 112 163 64 13;

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A; Accession: A49266
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-278 <SUD>
A; Cross-references: GB:U0
                                                                                                                                                                                                                                                                                                                                                                                                             R;Takahashi, T.; Tanaka, M.; Brannan, C.I.; Jenkins, N.A.; Copeland, Cell 76, 969-976, 1994
A;Title: Generalized lymphoproliferative disease in mice, caused by a A;Reference number: A53062; MUID:94185175
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fas ligand - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision
C;Accession: A53062
R;Takahashi, T.; Tanaka, M.; Brannan, C
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A; Residues: 1-279 <TAK>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVYVVKTSIKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PPPSPL-PPPSQPPPLPPLSPLKKKDNIELWLPVIFFMVLVALVGMGLG------MYQL
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                            HDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVYVVKTSIK
                                                                                        LQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLTIN--AASIPSGSHKVTLSSWY
                                                                                                                                                        YFRAQMDPNRISEDSTHCFYRILRLHENADLQDSTLESEDTLPDSCRRMKQAFQGAVQKE 107
                                                                                                                                                                                        PPVSPL-PPPSQPLPLPPLTPLKKKDHNTNLWLPVVFFMVLVALVGMGLG-----MYQ
                                                                                                                                                                                                                      PHEGPLHPAPSAPAPAPP------PAASRSMFLALLGLGLGQVVCSTALFL 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFG
DTYGTALISGVKYKKGGLVINETGLYFVYSKVYFR-GQSCNNQPLNH---KVYM--RNSK
                                                                                                                           LFHLQKE---LAE-----LREFTNQSLKVSSFEKQIANPST---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 177.5; DB 2;
Pred. No. 1.5e-07;
2; Mismatches 101;
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Pred. No. 1.7e-07;
6; Mismatches 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -SLRVSSFEKQIANPSTPSETK-
                                                               -KKEPRSVAHLTGNPHSRSIP
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                                                                                                                                                                                                                                                         97;
                                                                                                                                                                                                                                                                                                                                                                                                                                  mice, caused by a point mutation
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C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C;Accession: I38707; JC2340; S57555; I38554
R;Takahashi, T.; Tanaka, M.; Inazawa, J.; Abe, T.; Suda, T.; Nagata, S.
Int. Immunol. 6, 1567-1574, 1994
A;Title: Human Fas ligand: gene structure, chromosomal location and species
A;Reference number: I38707; MUID:95127560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:U11821; NID:g595430; PIDN:AAC50124.1; PID:g595431 R;Mita, E.; Hayashi, N.; Iio, S.; Takehara, T.; Hijioka, T.; Kasahara, A.; Fusam Biochem. Biophys. Res. Commun. 204, 468-474, 1994 A;Title: Role of Fas ligand in apoptosis induced by hepatitis C virus infection. A;Reference number: JC2340; MUID:95071350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:X89102; NID:g887455; PID:g887456
R;Alderson, M.R.; Tough, T.W.; Davis-Smith, T.; Braddy, S.;
J. Exp. Med. 181, 71-77, 1995
A;Title: Fas ligand mediates activation-induced cell death
A;Reference number: 138554; MUID:95105731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Schatzlein, C.E.
submitted to the EMBL Data
A;Reference number: S57565
A;Accession: S57565
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A; Residues: 1-281 <RE
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A; Residues: 1-281 <RE2>
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A; Residues: 1-281 <SCH>
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A; Residues: 1-281 <MIT>
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EKQIGHPSPPPE
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Pred. No. 3e-07;
13; Mismatches 1
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  KKELRKVAHLTGKSNSRSMP-
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C;Species: Homo sapiens (man)
C;Date: 02-ul-1996 #sequence_revision 02-Jul-1996 #text_change 20-Apr-2001
C;Accession: S28017; JH0793; S26694; S28852; I53476; S25684; S30593
R;Hollenbaugh, D.; Grosmaire, L.S.; Kullas, C.D.; Chalupny, N.J.; Braesch-Andersen, EMBO J. 11, 4313-4321, 1992
A;Title: The human T cell antigen gp39, a member of the TNF gene family, is a ligance A;Reference number: S28017; MUID:93049181
A;Accession: S28017
                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-261 <GAU>
A; Cross-references: EMBL:L07414;
A; Note: the sequence from Fig. 3
C; Genetics:
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C; Keywords: glycoprotein;
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A; Residues: 1-261 <GRA>
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J. Exp. Med. 176, 1543-1550, 1992
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A; Residues: 1-261 <HOL>
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Matches 75
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SPRSAATGLP--ISMKIFMYLLTVFLITQMIGSALFAVYLHRRLD--KIEDER---
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                                                                                                                     Score 169.5; DB 2
Pred. No. 6.6e-07;
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(Asn) (covalent) #status
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K;ALIACT, D.; Spriggs, .....

; COSMan, D.; Spriggs, .....

Nature 357, 80-82, 1992

A;Title: Molecular and biological characterization

A;Reference number: S21738; MUID:92244364

A:Accession: S21738
tumor necrosis factor alpha precursor N;Alternate names: cachectin; TNF alpha C;Species: Equus caballus (domestic hors C;Date: 10-Sep-1999 #sequence_revision 10;Accession: J01344 R;Su, X; Morris, D.D.; McGraw, R.A. Gene 107, 319-321, 1991
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A;Residues: 1-260 <ARM>
A;Cross-references: EMBL:X65453; NID:950351; PIDN:CAA46448.
C;Keywords: glycoprotein; transmembrane protein
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C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 05-Nov-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Accession: S2173 R; Armitage, R.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;Keywords: glycoprotein; transmembrane protein;23-46/Domain: transmembrane #status predicted <TMM>;47-260/Domain: extracellular #status predicted <EXT
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Best Local
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                                                                                                                                                                                                                      AANTHSSSQLCEQQ--SVHLGGVFELQAGASVFVNVTEASQVIHRVGFSSFGLLKL
                                                                                                                                                                                                                                                                                                                               SNGK-LRVNQDGFYYLYANICF-RHHETSGSVPTDYLQLMVYVVKTSIK--IPSSHNLMK 234
                                                                                                                                                                                                                                                                                                                                                                            --EKKENSF--EMQRGDEDPQIAAHVVSEA----NSNAASVLQWAKKGYYTMKSNLVML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         H--SSAKPCGQQSIHLGGVFELQPGASVFVNVTDPSQVSHGTGFTSFGLLKL
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                                                                                                                                                                                                                                                       GGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKV
                                                                                                                                                                                                                                                                                                ENGKQLTVKREGLYYVYTQVTFCSNREPSSQRP-----FIVGLWLKPSIGSERILLK
                                                                                                                                                                                                                                                                                                                                                                                                                   APAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHKVTLSSWYHDRGWAKISNMT-L 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                          -VNLHEDFVFIKKLKRCNKGEGSLSLLNCEEMRRQFEDLVKDITLNKE------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ILRLHEN----ADLQDSTLESEDTLPDSCRRMKQAFQGAVQ-----KELQHIVGPQRFSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -NLHEDFVFM-KTIQRCNTGERSLSLLNCEEIKSQFEGFV-KDIM-----LNKEETKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 153; DB 2; Pred. No. 1.7e-05;
                                                                                horse)
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                                                           10-Sep-1999
                                                                                                                   horse
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A;Cross-references: GB:M64087; NID:g16.
C;Comment: This protein is an importan
C;Genetics:
A;Gene: TNF-alpha
A;Introns: 62/3; 79/1; 95/1
C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxin; glyco;
F;78-334/Product: tumor necrosis facto:
F;19,20/Binding site: myristate (Lys)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:M20155
R;Shakhov, A. N.; Nedospasov, S.A.
Bioorg. Khim. 13, 701-705, 1987
A;Title: Molecular cloning of the genes coding
A;Reference number: S03791; MUID:87298639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Cloning and expression in Escherichia coli of the gene A;Reference number: A22908; MUID:88224564 A;Accession: A22908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Date: 31-Mar-1988 *sequence_revision 31-Mar-1988 *text_change 04-F C;Accession: A22908; S03791; A27303; A25164; A23127; A34251; I59058; R;Shirai, T; Shimizu, N.; Shiojiri, S.; Horiguchi, S.; Ito, H.
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A;Residues: 1-235 <SEM>
A;Residues: 1-235 <SEM>
A;Cross-references: GB:Y00467; NID:g54830; PIDN:CAA68530.1; PID:g54832
R;Pennica, D:, Hayflick, J.S.; Bringman, T.S.; Palladino, M.A.; Goedde.
Proc. Natl. Acad. Sci. U.S.A. 82, 6060-6064, 1985
                                                                                                                                                                              A; Title: Nucleotide sequence of the murine TNF locus, A; Reference number: A93679; MUID:88067722 A; Accession: A27303
                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:M38296; NID:9202086; PIDN:AAA40459.1; PID:9202087
A;Note: article in Russian with English abstract
R;Semon, D.; Kawashima, E.; Jongeneel, C.V.; Shakhov, A.N.; Nedospasov,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tumor necrosis factor alpha precursor - mouse N; Alternate names: cachectin; TNF alpha
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                                                                                                                                              A; Molecule type: DNA
                                                                                                                                                                                                                                                                                  R; Semon, D.; Kawashima, E.; Jongeneel, Nucleic Acids Res. 15, 9083-9084, 1987
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A; Residues: 1-235 <SHI>
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24.1%;
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                                                                                                                                                                                                                                                                                                                  C.V.;
                                                                                                                                                                                                                                                                                                                      Shakhov,
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9058; A36696
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                                                                                                                                                                                                                                                                                                                      S.A.
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                                              D.V.
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A; Residues: 1-235 < FRA>
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A; Residues: 1-23
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          tumor necrosis
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Best Local
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          factor
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          alpha
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R;Cseh, K.; Beutler, B.

J. Biol. Chem. 264, 16256-16260, 1989
A;Title: Alternative cleavage of the cachectin/tumor
A;Reference number: A34251; MUID:89380231
A;Accession: A34251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Caput, D.; Beutler, B.; Hartog, K.; Thayer, R.; Brown-
Proc. Natl. Acad. Sci. U.S.A. 83, 1670-1674, 1986
A;Title: Identification of a common nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;20/Binding site: myristate (Lys) (covalent) \#status predicted F;84/Binding site: carbohydrate (Ser) (covalent) \#status predicted F;86/Binding site: carbohydrate (Asn) (covalent) \#status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; F;80-235/product: tumor necrosis factor #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Sherry, B.; Jue, D.M.; Zentella, A.; Cerami, A. Biochem. Biophys. Res. Commun. 173, 1072-1078, 1990 A;Title: Characterization of high molecular weight
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-230, 'R', 232-235 <RES>
A; Cross-references: GB:M13049; NID:g202082; PIDN:AAA40457.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Fransen, L.; Muller, R.; Marmenout
Nucleic Acids Res. 13, 4417-4429, 19
A;Title: Molecular cloning of mouse
A;Reference number: A23127; MUID:852
A;Accession: A23127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:M11731; NID:g202084; PIDN:AAA R;Fransen, L.; Muller, R.; Marmenout, A.; Tavernier, Nucleic Acids Res. 13, 4417-4429, 1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Note: the first intron occurs in the 5'-untranslated region C;Superfamily: tumor necrosis factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: protein A; Residues: 80-85, 'X', 87-99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Reference number: A36696; MUID:91097531
A;Accession: A36696
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A;Accession: I59058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: protein A; Residues: 70-87 < CSE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;148-179/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Introns: 62/3; 81/1; 97/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:X02611; NID:g54844;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary; translated from GB/EMBL/DDB.
                                                                                                                                                                                                                                                                                                                                                        111 IVGPORF----SGAP---AMMEGSWLDVAQRGKPEAOPFAHLTINAASIPSGSHKVTLS- 162
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EVNLPKYLDFAESGQVYFG
                                             QVSNPSLLD-PDQDATYFG
                                                                                                                                                                                                      EWLSQRANALLANGMDLKDNQLVVPADGLYLVYSQVLFK---
                                                                                                                                                                                                                                                                                                       VIGPQRDEKFPNGLPLISSMAQTLTLRSSSQNSSD-KPVAHVVAN-----
                                                                                                RFAISYQEKVNLLSAVKSPCPKDTPEGAELKPW--
                                                                                                                                                                                                                                                    SWYHDRGWAKISN-MTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVYVVK 221
                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                 TSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISI 268
                                                                                                                                                                                                                                                                                                                                                                                                                                      9.4%;
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231
                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 146.5;
Pred. No. 5.
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                                                                                                                                                                                                                                                                                                                                                                                                             .2e-05;
les 67;
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                                                                                                      -YEPIYLGGVFQLEKGDQLSA
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der Heyden,
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    untranslated region

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                                                                                                      212
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precursor

baboon

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C; Species: Papio sp. (baboon)
C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2
C; Accession: S22052
R; Sanjanwala, M; Edwards, A.
submitted to the EMBL Data Library, September 1991
A; Description: Baboon Tumor Necrosis Factor Derived from Sequences of Ge
A; Reference number: S22052
A; Accession: S22052
A; Accession: S22052
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-233 <SAN>
A; Cross-references: EMBL: M52141; NID: 938159; PIDN: CAA44068.1; PID: 938160
C; Genetics:
C; Superfamily: tumor necrosis factor
C; Superfamily: carbohydrate (Ser) (covalent) #status predicted
F; 18,1081nddng site: carbohydrate (Ser) (covalent) #status predicted
F: 14,-177/Ni-nilfida honds: #status predicted
A; Molecule type: mRNA
A; Residues: 1-234 < NAS>
A; Cross-references: EMBL: X56756; NID: g297806; PI
A; Croung, A. J.; Hay, J.B.; Chan, J.Y.C.
Nucleic Acids Res. 18, 6723, 1990
A; Title: Primary structure of ovine tumor necros
A; Reference number: S13114; MUID: 91067496
A; Accession: S13114
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tumor necrosis factor alpha precursor - sheep %; Alternate names: cachectin; TNF alpha C; Species: Ovis orientalis aries, Ovis ammon aries C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 C; Accession: JH0529; 848118; S13114; S20661
                                                                                                                                                                                                                                        A;Cross-references: EMBL:x55152; NID:g1405; A;Experimental source: alveolar macrophage R;Nash, A.D.; Barcham, G.J.; Brandon, M.R.; Immunol. Cell Biol. 69, 273-283, 1991 A;Title: Molecular cloning, expression and c A;Reference number: $48118; MUID:92155784 A;Accession: $48118
                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-234 < GRE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gene 109, 203-210, 1991
A;Tille: Sequence of the cDNA encoding ovine tumor necrosis A;Reference number: JH0529; MUID:92112044
A;Accession: JH0529
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Best Local S
Matches 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HDRGWAKISN-MTLSNGKLRVNODGFYYLYANICFRHHETSGSVPTDYLQL-----M 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VIGPQREEFPKDPSLI--SPLAQAVRSSSRTPSDKPVAHVVAN----PQAEGQL---QWL 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NRRANALLANGVELRDNQLVVPSEGLYLIYSQVLFK----GQGCPSTHVLLTHTISRIAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D.R.
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Pred. No. 9.
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                                                                    necrosis
                                                                                                                                                                                                                                                                                   characterization
                                                                                                                                                                                                                                                                                                                                                                                PIDN:CAA38952.1;
                                                                                                                                                                                                                                                                                                                                     Andrews, A.E.
                                                                                                                                          PIDN:CAA40076.1;
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#text_change 04-Feb-2000
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C;Superfamily: tumor necrosis factor
                                                                                                                                                                                                                                                                                                                                                                                           C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;McGraw, R.A.; Coffee, B.W.; Otto, C.M.; Drews, Nucleic Acids Res. 18, 5563, 1990
A;Title: Gene sequence of feline tumor necrosis A;Reference number: S11688; MUID:91016860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tumor necrosis factor alpha precursor - cat
C;Species: Felis silvestris catus (domestic cat)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-19
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                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-233 <MCG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Reference number: A; Accession: S11688
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A; Residues: 1-62,64-234 <YOU>
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Best Local S
Matches 50
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                      216
                                                       105
                                                                                          162
                                                                                                                                                     102 GAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHKVTL 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     167 DRGWA-KISNMTLSNG-KLRVNQ-----DGFYYLYANICFRHH------ETSGSVP
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                    ---MVYVVK---
                                                 LS---RRANALLANGVELTDNQLKVPSDGLYLIYSQVLF----TGQGCPSTHVLLTHAIS 157
                                                                                   SSWYHDRGWAKISN-MTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQL----
                                                                                                                            GPQREELPH-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QLRWGDSYANALMANGVELKDNQLVVPTDGLYLIYSQVLFRGHGCPSTPLFLTHTISRIA 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VIGPQREEQSPA------GPSFNRPLVQ-TLRSSSQASNNKPVAHVVANISAPG 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TDYLQLMYYVVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQ
                                                                                                                                                                                            l Similarity 25.1
50; Conservative
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-TSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISI
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                                                                                                                                                                                                             Score 140;
Pred. No. 0.
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                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-Nov-1995 #text_change 04-Feb-2000
                                                                                                                      --SRTPSDKPVAHVVAN----PEAEGQLQR 104
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les 74;
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C;Species: Homo sapiens (man)
C;Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 08-Dec-2000
C;Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 08-Dec-2000
C;Accession: A93585; 336153; A93351; A44189; B61478; I53311; S62610; I54522; A01646; B23
R;Nedwin, G.E.; Naylor, S.L.; Sakaguchi, A.Y.; Smith, D.; Jarrett-Nedwin, J.; Pennica, I
Nucleic Acids Res. 13, 6361-6373, 1985
A;Title: Human lymphotoxin and tumor necrosis factor genes: structure, homology and chro
A;Reference number: A93585; MUID:86016093
A;Accession: A93585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-233 < RENN>
A; Residues: 1-233 < RENN>
A; Residues: 1-233 < RENN>
A; Rosidues: 1-233 < RENN>
A; Rosidues: 1-233 < RENN>
A; Rote: this protein was isolated from the monocyte-like cell line HL-60 from a pr
A; Note: this protein was isolated from the monocyte-like cell line HL-60 from a pr
A; Note: this protein was isolated from the monocyte-like cell line HL-60 from a pr
A; Note: this protein was isolated from the monocyte-like cell line HL-60 from a pr
A; Note: this protein was isolated from the monocyte-like cell line HL-60 from a pr
A; Note: this protein was isolated from the monocyte-like cell line HL-60 from a pr
A; Note: Malecular cloning of the complementary DNA for human tumor necrosis factor
A; Reference number: A44189; MUID:85142190
A; Molecular type: mRNA
A; Rocession: A44189
A; Molecular type: mRNA
A; Residues: 1-62,'S', 64-233 < WANN
A; Residues: 1-62,
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1992
R;Pennica, D.; Nedwin, G.E.; Hayflick, J.S.; Seeburg, P.H.; Derynck, R.; Palladino,
Nature 312, 724-729, 1984
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A;Title: Simultaneous production of natural human tumor necrosis factor-alpha, -beta and A;Title: Simultaneous production of natural human tumor necrosis factor-alpha, -beta and A;Reference number: A61478; MUID:88301617
A;Reference number: B61478
A;Molecule type: protein
A;Residues: 83-102;109-119;121-128,'x',130-131;142-144,'x',146,'xxx',150-152;159-174;180
A;Residues: 83-102;109-119;121-128,'x',130-131;142-144,'x',146,'xxx',150-152;159-174;180
A;Marmenout, A.; Fransen, L.; Tavernier, J.; Van Der Heyden, J.; Tizard, R.; Kawashima, Eur. J. Biochem. 152, 515-522, 1985
Eur. J. Biochem. 152, 515-522, 1985
A;Title: Molecular cloning and expression of human tumor necrosis factor and comparison A;Reference number: 153311; MUID:86030296
A;Residues: translated from GB/EMBL/DDBJ
A;Residues: 1-233 <MAR>
A;Residues: 1-233 <MARA <MARA
A;Residues: 1-234 <MARA
A;Residues: 1-244 <MARA
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A;Accession: A93351
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Nature Genet. 3, 137-145, 1993
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A; Residues: 1-233 <NED>
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A; Residues: 1-233 <IRI>
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A; Accession: S62610
A; Molecule type: pro
A; Residues: 77-99 <
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A;Experimental source: U-937 cells
R;Takakura-Yamamoto, R.; Yamamoto, S.; Fukuda, S.; Kurimoto, M.
Eur. J. Blochem. 235, 431-437, 1996
                                                                                                                                                                A; Title: O-Glycosylated species of natural A; Reference number: S62610; MUID:96202967
                                                                                                                                                    A; Reference number: S62610;
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                                                                                                                                                                                                                                  human tumor-necrosis
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Perrot, V.;
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                                                                                                                             A; Accession: A25454
                                                                                                                                                                                        A; Title: Molecular cloning a A; Reference number: A25454;
                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000
C;Accession: A25454; A25451; JS0727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N; Alternate names: cachectin; C; Species: Oryctolagus cunicu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
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                                                                                                                                                                                                                                                                                                                                                   R; Ito, H.; Yamamoto, S.; Kuroda,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tumor necrosis factor alpha precursor
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149-156, 1986

and expression; MUID:86219711

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Sakamoto,

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Kajihara,

J.; of

Kiyota, T.; Hayashi,

TNF alpha

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A;Contents: annotation; identification of myristy; R;Aggarwal, B.B.; Kohr, W.J.; Hass, P.E.; Moffat, J. Biol. Chem. 260, 2345-2354, 1985
A;Title: Human tumor necrosis factor. Production, A;Reference number: A92511; MUID:85130974
A;Contents: annotation; disulfide bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:S68530; NID:9544751
R;Stevenson, F.T.; Bursten, S.L.; Locksley, R.M.; Lovett, D.H.
J. Exp. Med. 176, 1053-1062, 1992
A;Title: Myristyl acylation of the tumor necrosis factor alpha
A;Reference number: A59163; MUID:93018820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;D'Alfonso, S.; Richiardi, P.M.
Immunogenetics 39, 150-154, 1994
A;Title: A polymorphic variation in a putative regulation
A;Reference number: I54522; MUID:94102809
A;Accession: I54522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxin; glycoprotein; homotrimer; lipoprotein;
F;1-76/Domain: propeptide #status predicted <PRO>
F;1-72/33/Product: tumor necrosis factor #status experimental <MAT>
F;19,20/Binding site: myristate (Lys) (covalent) #status experimental
F;81/Binding site: carbohydrate (Ser) (covalent) (partial) #status experimental
T;81/Binding site: carbohydrate (Ser) (covalent) (partial) #status experimental
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A; Introns: 62/3; 78/1; 94/1
C; Complex: homotrimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Comment: Secreted from mitogen-activated macrophages within 4-24 hours after in out detriment to normal cells. It can also act synergistically with interferon gac;Comment: TNF-alpha and -beta (lymphotoxin) are the products of different genes ut are produced by different cell types and have different induction kinetics.
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A; Residues: 1-8 < DAL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                     275
                                                                                                          164
                                                                                                                                                                                                                                                                    168
                                                                                                                                                                                                                                                                                                                                                                       111 IVGPORFSGAPAMMEGSWLDVAQRGK---PEAQPFAHLTINAASIPSGSHKVTLSSWYHD 167
217
                                                                                                                                                                                                                                                                                                                          55
                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
nes 48; Conser
                                                                                                    QTKVNLLSAIKSPCQRETPEGAEAKPW-----YEPIYLGGVFQLEKGDRLSAEINRPD
                                                                                                                                                                                                                                                                                                                       VIGPQREEFPRDLSLISPLAQAVRSSSRTPSDKPVAHVVAN----PQAEGQL----QWLNR 107
                                                  LLD-PDQDATYFG 286
                                                                                                                                                                                                                                                            RGWAKISN-MTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQL------MVY 218
  YLDFAESGQVYFG
                                                                                                                                                             VVK----TSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPS
                                                                                                                                                                                                                  RANALLANGVELRDNQLVVPSEGLYLIYSQVLFK---
                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                           8.9%;
24.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                               Score 139.5;
Pred. No. 0.00
34; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .0002;
                                                                                                                                                                                                                     -GQGCPSTHVLLTHTISRIAVSY 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
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                                                                                                                   216
                                                                                                                                                                     274
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C: Accession: 154490
R: Crew, M.D.; Filipowsky, M.E.;
Immunogenetics 35, 351-353, 199;
A: Title: Sequence of the tumor of A: Reference number: 154490; MUII
A: Accession: 154490
                                                                                                                                                                                                              tumor necrosis factor alpha precursor - white-footed mouse C;Species: Peromyscus leucopus (white-footed mouse) C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Introns: 62/3; 80/1; 96/1
C;Superfamily: tumor necrosis factor
C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine;
F;1-81/Domain: propeptide #status predicted <PRO>
F;82-234/Product: tumor necrosis factor #status predicted <MAT>
F;19,20/Binding site: myristate (Lys) (covalent) #status predicted
F;89/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;147-178/Disulfide bonds: #status predicted
                                                                  A; Status: preliminary; translated
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                                 A; Molecule type:
A; Residues: 1-235
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A:Title: Structural analysis of the rabbit TNF locus, A;Reference number: JH0309; MUID:91065534
A:Accession: JS0727
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-62, 'Q', 63-234 <SHA>
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;Cross-references: GB:M59233; NID:g202506; PIDN:AAA40596.1; PID:g202507
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-234 <IT2>
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R;Itc, H.; Shirai, T.; Yamamoto, S.; Akira, M.; Kawahara, S.; Todd, C.W.;
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Best Local
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157-165, 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----GSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLD-PDQDATYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHKVTLSSWYHDRGWAKISN-MTL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PNNLHLV-----NPVAQMVTLRS------ASRALSDKPLAHVV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EDSTHCFYRILRLHENADLQDSTLESEDTLPDSCRRMKQAFQGAVQKELQHIVGPQRFSG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EGPL-----PKKAGGPQGSKRCLCLSLESFLLVAGATTLFC----LLHERVIGPQEEES
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                                   1-235 <RES>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 22.6
68; Conservative
                                                       DNA
                                                                                                                                                         351-353, 1992
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                                                                                                               tumor necrosis factor/cachectin
90; MUID:92218012
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 137.5; DB 1;
Pred. No. 0.0003;
"" matches 99;
                                                                       from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SGQGCRSYVLLTHTVSRFAVSYPNKVNLLSAIKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----LQWLSQRANALLANGMKL 121
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C;Accession: 146047; S24642
R;Cludts, I.; Cleuter, Y.; Kettmann, R.; Burny, A.; Droogmans, Cytokine 5, 336-341, 1993
A;Title: Cloning and characterization of the tandemly arranged A:Reference number: 146046; MUID:94083525
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                                                                                                                                                                                                                                                                                                                                                      C;Superfamily: tumor necrosis factor (C;Keywords: glycoprotein; lipoprotein; myristylation; transmembrane F;20/Binding site: myristate (Lys) (covalent) #status predicted F;81/Binding site: carbohydrate (Ser) (covalent) #status predicted F;145-177/Disulfide bonds: #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tumor necrosis factor alpha precursor - bovine C:Species: Bos primigenius taurus (cattle) C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change C:Accession: I46047; S24642
                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Introns:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-233 <C
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A;Gene: PlTNF
A;Introns: 62/3; 81/1; 97/1
C;Superfamily: tumor necrosis factor
C;Keywords: glycoprotein; lipoprotein; myristylation
F;19,20/Binding site: myristate (Lys) (covalent) #status
F;84/Binding site: carbohydrate (Ser) (covalent) #status
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                                                                                                                     QLRWWDSYANALMANGVKLEDNQLVVPADGLYLIYSQVLFRGQGCPSTPLFLTHTISRIA
                                                   VSY-QTKVNIL-SAIKSPCHRETPEWAEAKPW--
                                                                                                                                                                                              VIGPQREESPGGPSI--NSPLVQTLRSSSQASSNKPVAHVVAD-----
                                                                                                                                                           HDRGWAKISNMTLSNG-KLRVNQ-----DGFYYLYANICFRHH----
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25.1%;
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Pred. No. 0.
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1; Mismatches 68;
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Search completed: July 8, 2002, 20:02:22 Job time: 4231 sec

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Copyright (c) 1993 - 2000 Compugen
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8 h tumor nec
1 homo sapien
2 mus musculu
9 bos taurus
0 rattus norv
7 mus musculu
3 homo sapien
5 felis silve
5 cavia porce
6 canis famil
8 mus musculu
3 equus cabal
7 macaca fasc
4 macaca fasc
4 macaca mula
4 mus musculu
0 papio banad
0 papio sp. (
1 ovis aries
1 felis silve
5 canis famil
5 homo sapien
4 oryctolagus
9 peromyscus
7 homo sapien
9 bos taurus
3 sus scrofa
4 marmota mon
9 rattus norv
5 mus musculu
3 cervus elap
6 homo sapien
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SEQUENCE FROM TISSUE-Thymic MEDLINE-980329 Anderson D.M., Tometsko M.E.,	SEQUENCE FROM N.A. TISSUE-Bone marrow stroma MEDLINE-98188248; PubMed- Yasuda H., Shima N., Naka. Mochizuki SI., Tomoyasu Mochizaki SI., Tomoyasu Morinaga T., Higashio K., "Osteoclast differentiati Osteoprotegerin/osteoclas to TRANCE/RANKL."; Proc. Natl. Acad. Sci. U.; [4]	SEQUENCE FROM N.A. TISSUE-Bone marrow; MEDLINE-98227661; PubMed-9568710; Lacey D.L. Timms E., Tan HL., Kelle Burgess T., Elliott R., Colombero A., Sullivan J., Hawkins N., Davy E., Capp, Kaufman S., Sarosi I., Shalhoub V., Se Boyle W.J.; "Osteoprotegerin ligand is a cytokine differentiation and activation."; Cell 93:165-176(1998). [3]	Mammalia; Eutheria; NCBI_TaxID=10090; [1] TaxID=10090; [1] SEQUENCE FROM N.A. TISSUE-Hybridoma; MEDLINE=97460112; P Wong B.R., Rho J., Kalachikov S., Cayan Choi Y.; TRANCE is a novel that activates c-Ju J. Biol. Chem. 272; [2]	I I MOUSE 1235 0353 0027-2001 0027-2001 0027-2001 increase rule of the control of	115.5 109.5 109.1 109 104.5 101.5 97 93.5 92.5 92.5 98.5
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	stroma; PubMed=9 1. Nakag 1. Nakag Omoyasu shio K., centiatio teoclast	PubMed-S E. Tan Lt., Tan Lt., Ch Li., Sha Liyand is nd activa	A. PubMed=9312 PubMed=9312 Arron J. Yani E. Bar Jun N-termin 72:25190-2519	ANDARD; 40, Crei 40, Lass 40, Lass ctor ligg kappa B (TRANCE CTRANCE OR TRANCI OR TRANCI	193 233 201 340 450 450 205 197 1697 1697 202 1547
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ö; Billingsley M.C., DuBos	ramino K. Na N. Na N), Kelley TO A., E. Cappaı V., Send	ciurognal 2; sett F.S. ettmor r kinase i kinase i	RT; ence u tation perfam perfam objection RA OSteoc	TNFA_CAPHI TNFA_MACEU TNFB_MACEU TNFB_MACEU TNFD_TMOUSE YK22_YEAST TNFB_RABIT SN_MOUSE POLG_TBEVH TNFB_MOUSE RRPO_PMV ALIGNMEN
gsley W.L., Dougall u DuBose R.F., Cosman	guchi K., Kinosa Goto M., Muraka Takahashi N., Su a ligand for ibitory factor a	y M.J., Dunstan Elliott G., Scul arelli C., Eli A naldi G., Guo J.	E., Orlinick J. III, Frankel necrosis facto	6 AA. ate) podate) y member 11 (R y member 11 (R continue of the continue of	MENTS
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•	Tsuda E., identical	i., Hsu H., Jian YX., Jianey J.,	, Mus.	activator ation- Osteoclast factor)	capra hircu macropus eu macropus eu sacroharomyc mus musculu saccharomyc homo sapien oryctolagus mus musculu t genome po mus musculu papaya mosa

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[5]
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CONFLICT
SEQUENCE
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Interpro; IPR003263; TNF_5.
Interpro; IPR000478; TNF_family.
Pfam; PF00229; TNF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF013713; AAC40113.1; -. EMBL; AF013170; AAC71061.1; -. EMBL; AB0008426; BAA25425.1; -. EMBL; AF019048; AAB86812.1; -. EMBL; AB036798; BAA97259.1; -.
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entities requires a license agreement (See http://www.isb-
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                                                                                                                                                                                                                                                                                                                                       Cytokine;
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                                                                                                                                                                                                                                              CARBOHYD
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                                                                                                                                     Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
FUNCTION: OSTEOCLAST DIFFERENTIATION AND ACTIVATION FACTOR.
AUGMENTS ABILITY OF DENDRITIC CELLS TO STIMULATE NAIVE T-CELL PROLIFERATION. MAY BE AN IMPORTANT REGULATOR OF INTERACTIONS BETWEEN T CELLS AND DENDRITIC CELLS AND MAY PLAY A ROLE IN THE REGULATION OF THE T CELL-DEPENDENT IMMUNE RESPONSE.
REGULATION OF THE T CELL-DEPENDENT IMMUNE RESPONSE.
RUGGLIULAR LOCATION: Type II membrane protein (Potential).
TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THYMIS AND LYMPH NODES NOT IN NONLYMPHOID TISSUES AND IS ABUNDANTLY EXPRESSED IN THE BUT NOT IN B CELLS. A HIGH LEVEL EXPRESSION IS ALSO SEEN IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BUT NOT IN B CELLS. A HIGH LEVEL EXPRESSION IS ALSO SEEN IN THE TRABECULAR BONE AND LUNG.

TRABECULAR BONE AND LUNG.

DISEASE: DEFICIENCY IN THESF11 RESULTS IN FAILURE TO FORM LOBULO-
BLYDOLAR MAMMARY STRUCTURES DURING PREGNANCY, RESULTING IN DEATH
OF NEWBORNS. TRANCE-DEFICIENT MICE SHOW SEVERE OSTEOPETROSIS, WITH
NO OSTEOCLASTS, MARROW SPACES, OR TOOTH ERUPTION, AND EXHIBIT
PROFOUND GROWTH RETARDATION AT SEVERAL SKELETAL SITES, INCLUDING
THE LIMBS, SKULL, AND VERTEBRAE AND HAVE MARKED CHONDRODYSPLASIA,
WITH THICK, IRREGULAR GROWTH PLATES AND A RELATIVE INCREASE IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYPERTROPHIC CHONDROCYTES.
SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
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                                                        GVPHEGPLHPAPSAPAPAPPPAASRSMFLALLGLGLGQVVCSIALFLYFRAQMDPNRISE
DSTHCFYRILRLHENAGLQDSTLESEDTLPDSCRRMKQAFQGAVQKELQHIVGPQRFSGA
                390:175-179(1997).
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                                                                                                                                                                                                                                                                                                                                      Differentiation; Receptor; Glycoprotein; Transmembrane;
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262
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N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
G -> D (IN REF. 4).
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Tometsko M.E., 1
Galibert L.;
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014788; 014723; 099203;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Tumor necrosis factor ligand superfamily member 11 (Receptor activator of nuclear factor kappa B ligand) (RANKL) (TMF-related activation-induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Osteoclast differentiation factor) (ODF).
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Mammalia; Eutheria;
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Kalachikov S., Cayani E., Bartlett F.S. III, Frank
                                                                                                                                                                                                                                                                                                                      differentiation and ac Cell 93:165-176(1998).
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MEDLINE=98227661;
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MEDLINE=97460112;
                                                                                                                                                                                                                                                                                             SEQUENCE OF 73-317 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature
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                                                                            encoding
                                                                                                                    TISSUE=Tongue;
MEDLINE=20175237;
                                                                                                                                                  SEQUENCE FROM
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                                                                           "Cancer cells responsible encoding a secreted form c
                                                                                                                                                                           "TRANCE is a novel ligand of the tumor necrosis factor receptor family that activates c-Jun N-terminal kinase in T cells.";
J. Biol. Chem. 272:25190-25194(1997).
                                                             formation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         homologue of the TNF receptor and
UNEM. BIOPHYS. RES. COMMUN. 269:532-536(2000).
FUNCTION: OSTEOCLAST DIFFERENTIATION AND ACTIVATION FACTOR.
AUGMENTS ABILITY OF DENDRITIC CELLS TO STIMULATE NAIVE T-CELL
PROLIFERATION. MAY BE AN IMPORTANT RECUIRATION.
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ROUX E.R., Teepe M.C., DuBose R.F.,
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Catarrhini;
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F/TRANCE that induces
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Frankel W.
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                                                                                 osteoclast
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.N., I
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Matches 250
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VARSPLIC
CONFLICT
SEQUENCE
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-1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (ISOFORM 1) AND SECRETED (ISOFORM 2).

-1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2/SODF; ARE PRODUCED BY ALTERNATIVE SPLICING.

-1- PRODUCED BY ALTERNATIVE SPLICING.

-1- TISSUE SPECIFICITY: HIGHEST IN THE PERIPHERAL LYMPH NODES BUT WEAK IN SPLEEN, PERIPHERAL BLOOD LEUKOCYTES, BONE MARROW, HEART, PLACENTA, SKELETAL MUSCLE, STOMACH AND THYROID.

-1- INDUCTION: UPREGULATED BY T CELL RECEPTOR STINULATION.

-1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR003263; TNF_5.
InterPro; IPR000478; TNF_family.
Pfam; PF00229; TNF; 1.
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SNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVYVVKTSIKIPSSHNLMKGGST
                                                                                                                                                                                                                                                                                                                        GAPHEGPLH-APPPPAPHQPPAASRSMEVALLGLGLGQVVCSVALFFYFRAQMDPNRISE
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                                                                                                                                                                                                                                         DSTHCFYRILRLHENADLQDSTLESEDT--LPDSCRRMKQAFQGAVQKELQHIVGPQRFS
                                                                                SNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMVYVTKTSIKIPSSHTLMKGGST
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psforentiation; Recepto
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317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MW;
                                                                                                                                                                                                                                                                                                                                                                                                               16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-STANG (IN ISOFORM 2).

A -> G (IN REF. 3).

M; 766176446348097F CRC64;
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6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1326.5;
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SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN)
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L.8e-107;
                                                                                                                                                                                                                                                                                                                                                                                                             27;
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EMBL; U37518;
EMBL; U57059;
MIM; 603598; -
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01-OCT-1996 (Rel. 34, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Tumor necrosis factor ligand superfamily membe
apoptosis inducing ligand) (TRAIL protein) (Ar-
TNFSF10 OR TRAIL OR APO21.
                        Pfam; PF00229; TNF; 1.
                                    InterPro;
InterPro;
                                                                                                                                                        use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                           This
                                                                                                                                                                                                                                                                                      -i- FUNCTION: INDUCES APOPTOSIS.
-i- SUBUNIT: HONOTRIMER (POTENTIAL).
-i- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
-i- TISSUE SPECIFICITY: WIDESPREAD; MOST PREDOMINANT IN SPLEEN,
                                                                                                                                                                                                                                                                                                                                              PubMed=10542098;
Mongkolsapaya J., Grimes J.M., Chen N., Xu X Jones E.Y., Screaton G.R.;
"Structure of the TRAIL-DR5 complex reveals specificity in apoptotic initiation.";
Nat. Struct. Biol. 6.1048-1053/1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hymowitz S.G., Christinger H.W., Fuh G., Ultsch M., O'Connell M., Kelley R.F., Ashkenazi A., de Vos A.M.;
"Triggering cell death: the crystal structure of Apo2L/TRAIL in a complex with death receptor 5.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

MEDLINE-96111955; PubMed-8777713;

Wiley S.R., Schooley K., Smolak P.J., Din W
Micholl J.K., Sutherland G.R., Davis-Smith
Goodwin R.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TN10_HUMAN
P50591;
01-OCT-1996
           ProDom;
                                                                                                                                                                                                           between the Swiss Institute of Bioinf
the European Bioinformatics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF MEDLINE=20017054; PubMed=10549288;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Placenta;
MEDLINE=96278649; PubMed=8663110;
                                                                                                                                                                                                                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pitti R.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Identification and characterization of a family that induces apoptosis."; immunity 3:673-682(1995).
                                                                 interPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Induction of apoptosis by Apo-2 ligand, necrosis factor cytokine family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
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                                ; 1D0G; 22-OCT-99.

;; 1D4V; 01-NOV-99.

:erPro; IPR003263; TNF_abc.

:erPro; IPR003636; TNF_family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    crosis factor cytokine family.";
Biol. Chem. 271:12687-12690(1996).
                                                                                                                                                                                                                                                                AND PROSTATE.
SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
                                                                                                                                                                                                                        SWISS-PROT entry is copyright. It is produced through a een the Swiss Institute of Bioinformatics and the EMBI
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cell 4:563-571(1999).
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                                                                                                                  AAC50332.1;
AAB01233.1;
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         TNF_abc; 1.
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Primates;
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Catarrhini;
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i; Hominidae;
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C., Smith C./
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RESULT 4
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Best L
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                                                                                                                           "Identification and characterization of family that induces apoptosis."; Immunity 3:673-682(1995).
-!- FUNCTION: INDUCES APOPTOSIS.
-!- SUBUNIT: HOMOTRIMER (POTENTIAL).
-!- SUBCELLULAR LOCATION: Type II memb.
-!- TISSUE SPECIFICITY: WIDESPREAD.
-!- TISSUE SPECIFICITY: WIDESPREAD.
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SEQUENCE
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                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=96111955; PubMed=8777713;
Wiley S.R., Schooley K., Smolak P.
Nicholl J.K., Sutherland G.R., Dav
Goodwin R.G.;
                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Tumor necrosis factor ligand superfamily member
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                     P50592;
01-OCT-1996 (Rel.
                      modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboratement he Swiss Institute of Bioinformatics and the EMBL outstatthe European Bioinformatics Institute. There are no restrictions on
                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                                                                                 apoptosis inducing ligand) (TRAIL
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EMBL;
                                                               use
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U37522;
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39
AAC52345.1;
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2; 1.
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ne; Signal-anchor; Apoptosis; 3D-strune; Signal-anchor; CPOTENTIAL).
7 CYTOPLASMIC (POTENTIAL).
81 EXTRACELLULAR (POTENTIAL).
81 EXTRACELLULAR (POTENTIAL).
97509 MW; DDAAAF78DAAB2F6D CRC64;
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TO THE TUMOR NECROSIS FACTOR FAMILY.
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Pred. No. 3.6e-15;
4; Mismatches 113;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cytokine; Transmembrane; Si
DOMAIN 1 17
TRANSMEM 18 38
DOMAIN 39 291
CARBOHYD 52 52
SEQUENCE 291 AA; 33477 M
                                                                                                                                                                                                                                                 01-OCT-1996
01-OCT-1996
30-MAY-2000
CD40 ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SMUJUU, ..., TNE_1; 1.

PROSITE; PS00251; TNE_1; 1.

PROSITE; PS50040; TNE_2; 1.

PROSITE; PS50040; TNE_2; 1.

PROSITE; PS50040; TNE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00229; TNF; 1.
ProDom; PD002012; TNF_abc; 1.
ProDom; PD00860; TNF_5; 1.
SMART; SM00207; TNF; 1.
                                                                                                                                                                                                                                                                                                      TNF5_BOV
P51749;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003636; TNF_abc.
InterPro; IPR000478; TNF_family.
MEDLINE-96005582; PubMed=7590981;
Mertens B.E.L.C., Muriuki M., Gaidulis L.;
Mertens B.E.L.C., Muriuki M., Gaidulis L.;
"Cloning of two members of the TNF-superfamily in cattle: CD40 li
"cloning of two members of the TNF-superfamily in cattle: CD40 li
and tumor necrosis factor alpha.";
Immunogenetics 42:430-431(1995).
Inmunogenetics 42:430-431(1995).
Inmunogenetics 42:430-431(1995).
Inmunogenetics 42:430-431(1995).
INTOLYBE AS WELL AS IGE PRODUCTION IN THE PRESENCE OF IL-4.
INVOLVED IN IMMUNOGLOBULIN CLASS SWITCHING (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGD; MGI:107414; Tnfsf10.
InterPro; IPR003263; TNF_5
                                                                                                                                                   Bovidae; Bovinae; NCBI_TaxID=9913;
                                                                                                                                                                                Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniai
Mammalia; Eutheria; Cetartiodactyla;
                                                                                                                                                                                                                        TNESES OR CD40LG
                                                                                                                                                                                                                                                                                                                                    BOVIN
                                                                                                              TISSUE=Blood;
                                                                                                                                                                                                                                      GP39)
                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RLHENADLODSTLESEDTLPDSC----RRMKQAFQGAVQKELQHIVG--PQRFSGAPAMM 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALKDLSFSQHFRMMVICIVLLQVLLQAVSVAVTYMYFTNEMKQLQDNYSKIGLACFSK--
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                                                                                                                                                                                                                                                                                                                                                                                                                  ?
                                                                                                                                                                                                                                                                                                                                                                                                                                             PIVLMKSARNSCWSRDAEYGLYSIYQGGLFELKKNDRIFVSVTNEHLMDLDQEASFFGAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HVLFRNGELVIEQEGLYYIYSQTYFRFQEAEDASKMVSKDKVRTKQLVQYIYKYT-SYPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NMTLSNGKLRVNQDGFYYLYANICFRHHE---TSGSVPTDYL---QLMVYVVKTSIKIPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EGSWLDVAQRGKPEAQPFAHLT----INAASIPSGSHXVTL----SSWYHDR-GWAKIS
                                                                                                                                                                                                                                                                                                                      BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84;
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                                                                                                                                                                                                                                                                                                                                                                                        290
                                                                                                                                                                                                                                                                                                                                                                                                                   290
                                                                                                                           FROM
                                                                                                                                                                                                                                                 (Rel. 34, Created)
(Rel. 34, Last sequence up
(Rel. 39, Last annotation
(TNF-related activation pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                            N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -GRPQ-KVAAHITGITRRSNSALIPISKDGKTLGQKIESWESSRKGHSFLN
                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                         OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --DGEILNRPCLQVKRQLYQLIEEVTLRTFQDTISTVPEKQLSTPPLP
                                                                                                                                                                   Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16.1%;
27.8%;
                                                                                                                                                                                                                        CD40L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 251; DB 1;
Pred. No. 1.7e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II ME
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-LINKED (GLCNAC
                                                                                                                                                                                               Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3FEACAB9F0D7D802 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----FLYFRAQMD--PNRISEDSTHCFYRIL
                                                                                                                                                                                                                                                    protein)
                                                                                                                                                                                                                                                                              update
                                                                                                                                                                                  Ruminantia; Pecora;
                                                                                                                                                                                                                                                                                                                        261
                                                                                                                                                                                                                                                                 update)
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                                                                                                                                                                                               Euteleostomi;
                                                                                                                                                                                                                                                       cell antigen
                                                                                                                                                                                    Bovoidea;
                                                                          CD40 ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          169
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RESULT
FASL_RAT
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Best Local S
Matches 71
                                             OlJUN-1994 (Rel. 29, Created)
OlJUN-1994 (Rel. 29, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
FAS antigen ligand.
TMFSF6 OR APTILG1 OR FASL.
Rattus norvegicus (Rat).
Eukaryota; Mctazoa; Chordata; Craniata; Verte
Mammalla; Eutheria; Rodentia; Sciurognathi; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
DISULFID
CARBOHYD
SEQUENCE
                                                                                                                                                        P36940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
SEQUENCE FROM N.A. MEDLINE-94084792;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; 1... TNF; 1. Pfam; PF00229; TNF; 1.
                                     NCBI_TaxID-10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00207; TNF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; Z48469; CAA88363.1; -.
HSSP; P29965; IALY.
InterPro; IPR003263; TNF_5.
InterPro; IPR00478; TNF_family.
                                                                                                                                                                        FASL_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cytokine;
                                                                                                                                                                                                                                                                                                                                          113
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                                                                                                                                                                                                                                      214
                                                                                                                                                                                                                                                               243
                                                                                                                                                                                                                                                                                         164
                                                                                                                                                                                                                                                                                                                 186
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SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT: HON
                                                                                                                                                                                                                                                  GNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKV
                                                                                                                                                                                                                                                                                                     NQDGFYYLYANICF-RHHETSGSVPTDYLQLMYYVVKTSIKIPSSHN--LMKGGSTKNWS
                                                                                                                                                                                                                                                                                       KRQGFYYIYTQVTFCSNRETLSQAP
                                                                                                                                                                                                                                                                                                                                                                                             FMKTIQRCNKGEGSLSLL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PAPSAPAPAPPPAASRSMFLALLGLGLGQVVCSIALF-LYFRAQMDPNRISEDSTHCFYR
                                                                                                                                                                                                                                  SKPCGQQSIHLGGVFELQSGASVFVNVTDPSQVSHGTGFTSFGLLKL
                                                                                                                                                                                                                                                                                                                                                                LDVAQRGKPEAQPFAHLTINAASIPSGSHKVTLSSWYHDRGWAKISN--MTLSNGK-LRV
                                                                                                                                                                                                                                                                                                                                       ---MHKGDQEPQIAAHV-----ISEASSKTTSVLQWAPKGYYTLSNNLVTLENGKQLAV
                                                                                                                                                                                                                                                                                                                                                                                                                 ILRLHENADLQDSTLESEDTLPDSCRRMKQAFQGAVQKELQHIVGPQRFSGAPAMMEGSW 128
                                                                                                                                                                                                                                                                                                                                                                                                                                             PSPRSVATGPP--VSMKIFMYLLTVFLITQMIGSALFAVYLHRRLDKIE-DERNLHEDFV 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PS00251; TNF_1; 1.
PS50049; TNF_2; 1.
PS50049; TNF_2; 1.
CYTOPLASMIC (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
23 46 CYTOPLASMIC (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47
178
240
261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HOMOTRIMER
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                                                                                                                                                                    STANDARD;
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218
240
29242 N
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PubMed=7505205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11.98;
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EXTRACELLULAR (POTENTIAL).

POTENTIAL.

N-LINKED (GLCNAC. . ) (POTENTIAL).

W; 8491FEFB30A787FD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                           -NCEEIRSRFEDLVKDIMQN----KEVKKKEKNFE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 185.5; DB 1
Pred. No. 6.8e-09;
4; Mismatches 122
                                               Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                     -----FIASLCLKSPSGSERILLRAANTH--S
                                                                                                                                                                    278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
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                                                                                                                                                                                                                                                          290
                                                                                                                                                                                                                                   261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41;
                                                 Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Best Local S
Matches 70
                                                                                                                                                                                                                                                                                         CARBOHYD
CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                           TRANSMEM
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                 Cytokine; Transmembrane; DOMAIN 1 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Suda T., Takahashi T., Golstein P., Nagata S.;

"Molecular cloning and expression of the Fas ligand, a novel member
of the tumor necrosis factor family.";
Cell 75:1169-1178(1993).

-I- EUNCTION: CYTOKINE THAT BINDS TO FAS ANTIGEN, A RECEPTOR THAT
TRANSDUCES THE APOPTOTIC SIGNAL INTO CELLS. MAY BE INVOLVED IN
CYTOTOXIC T CELL MEDIATED APOPTOSIS AND IN TELL SUBJECTION OF
PAS-ANTIGEN MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF
PAS-ENTREAL TOLERANCE, IN THE ANTIGEN-STIMULATED SUICIDE OF MATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00229; TNF; 1.
ProDom; PD002012; TNF_abc;
ProDom; PD008600; TNF_5; 1
SMART; SM00207; TNF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entitles requires a license agreement (See http://www.isborsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00251; TNF_1; PROSITE; PS50049; TNF_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003263; TNF_5.
InterPro; IPR003636; TNF_abc.
InterPro; IPR000478; TNF_family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; P01375; 4TSV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U03470; AAC52129.1; -.
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     162
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                              167
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                                                                                                                                                                   50
                                                                                                                                                                            3 PHEGPLHPAPSAPAPAPP-------PAASRSMFLALLGLGLGQVVCSIALFLY 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SURFACE.
TISSUE SPECIFICITY: EXPRESSED IN ACTIVATED SPLENOCYTES
THYMOCYTES. MODERATE OR WEAK EXPRESSION FOUND IN SMALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KIDNEY AND LUNG.
INDUCTION: BY PMA/IONOMYCIN
SIMILARITY: BELONGS TO THE T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T CELLS, OR BOTH.
SUBUNIT: HOMOTRIMER (PROBABLE).
SUBCELLULAR LOCATION: TYPE II M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MAY BE INTO THE EXTRACELLULAR FLUID, PROBABLY BY CLEAVAGE FORM
              DRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVVVVKTSIKI
                                                                    QHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLTIN--AASIPSGSHKVTLSSWYH
TYGTALISGVKYKKGGLVINEAGLYFVYSKVYFR-GQSCNSQP---
                                                                                                                                 FRAQMDPNRISEDSTHCFYRILRLHENADLQDSTLESEDTLPDSCRRMKQAFQGAVQKEL 108
                                                                                                          FHLQKELAELREFTNH------SLRVSSFEKQIANPSTPSETK------
                                                                                                                                                                PPPSPL-PPPSQPPPLPPLSPLKKKDNIELWLPVIFFMVLVALVGMGLG-----
                                                                                                                                                                                                                       70;
                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                         78
100
4
5
199
116
247
257
                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                  99
278
69
58
230
116
247
247
257
257
                                                                                                                                                                                                                                  11.4%; 23.0%;
                                                                                                                                                                                                                                                                                                                                                            ; 1.
; 1.
; 1.
; Glycoprotein; Signal-anchor; Apoptosis.
CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
TYTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                          W.
                                                                                                                                                                                                                    42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <u>-</u>
                                                                                                                                                                                                                                                                                       POLY-PRO.
BY SIMILARITY.
N-LINKED (GLCNAC. ..) (
N-LINKED (GLCNAC. ..) (
N-LINKED (GLCNAC. ..) (
N-LINKED (GLCNAC. ..) (
2898E18A862CEAC6 CRC64
                                                                                                                                                                                                                    Score 177.5; I
Pred. No. 3.6e
42; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TUMOR NECROSIS FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AND
                                                      KPRS--VAHLTGNPRSRSIP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONCAVALIN/INTERLEUKIN-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                    .6e-08;
                                                                                                                                                                                                                                               ВВ
                                                                                                                                                                                                                    101;
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                                                                                                                                                                                                                                                                                                   (POTENTIAL)
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INTESTINES,
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FASL_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P41047; Q61217; Q9R1F2;
01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
FAS antigen ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tough T., Gibson M., payes small mutated in "The mouse Fas-ligand gene is mutated in TNF family gene cluster."; Immunity 1:131-136(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [3]
SEQUENCE FROM N.A. (ISOFORM FASL).
MEDLINE-95196085; PubMed-7889405;
Lynch D.H., Watson M.L., Alderson M.R., Baum
Tough T., Gibson M., Davis-Smith T., Smith C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Comparative molecular modelling of the TNF family."; Mol. Immunol. 32:761-772(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
               MEDLINE-96091792; PubMed-7495745;
Hahne M., Peitsch M.C., Irmler M., Schroeter M., Lowin B.,
Rousseau M., Bron C., Renno T., French L., Tschopp J.;
"Characterization of the non-functional Fas ligand of gld mice.";
Int. Immunol. 7:1381-1386(1995).
-i- FUNCTION: CYTOKINE THAT BINDS TO FAS ANTIGEN, A RECEPTOR THAT
TRANSDUCES THE APOPTOTIC SIGNAL INTO CELLS. MAY BE INVOLVED IN
CYTOTOXIC T CELL MEDIATED APOPTOSIS AND IN T CELL DEVELOPMENT.
FAS-ANTIGEN MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION
                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORM FASLS).

STRAIN-C3H; TISSUE-Speleen;

MEDLINE-20021694; PubMed-10552956;

MEDLINE-20021694; PubMed-10552956;

Ayroldi E., D'Adamio F., Zollo O., Agostini M., Moraca R.,

Cannarile L., Migliorati G., Delfino D.V., Riccardi C.;

"Cloning and expression of a short Fas ligand; A new alternatively

spliced product of the mouse Fas ligand gene.";

Blood 94:3456-3467(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Generalized lymphoproliferative mutation in the Fas ligand.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE=94185175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=C57BL/6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Suda T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Takahashi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TNFSF6 OR APTILG1 OR FASL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FASL_MOUSE
                                                                                                                                                                                                                  CHARACTERIZATION OF VARIANT GLD.
MEDLINE=96091792; PubMed=7495745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fenner M.H., Shioda T., Isselbacher K.J
"Mus musculus Balb/c Fas ligand differs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-BALB/C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peitsch M.J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MAY-1996) to the EMBL/GenBank/DDBJ
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PubMed=7511063;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Muridae; Murinae;
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EMBL; U10984; AAA19778.1; --
EMBL; S76752; AAB33780.1; --
EMBL; U58995; AAB03915.1; --
EMBL; AF119335; AAD52106.1;
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PROSITE; PS50049; TNF_2; 1.
PROSITE; PS50049; TNF_2; 1.
PROSITE; PS50049; TNF_2; 1.
PROSITE; PS50049; TNF_2; 1.
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Interpro; IPR003636; TNF_abc...
Interpro; IPR000478; TNF_family.
Pfam; PF00229; TNF; 1.
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SUBGURIT: HOMOTRIMER (PROBABLE).
SUBGURIT: HOMOTRIMER (PROBABLE).
SUBGURIT: HOMOTRIMER (PROBABLE).
SUBGURITE HOMOTRIMER (PROBABLE).
ISOFORM FASLS IS SOLUBLE.
ALTERNATIVE PRODUCTS: 2 ISOFORMS; FASL (SHOWN HERE) AND FARDUCED BY ALTERNATIVE SPLICING. ISOFORM FASL MEDIATES F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - puropean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in on way ified and this statement is not removed. Usage by and for commercial ities requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISEASE: A DEFICIENCY IN THIS PROTEIN IS THE CAUSE OF GENERAL LYMPHOPROLIFERATION DISEASE (GLD), AN AUTOSOMAL RECESSIVE DIRESPONSIBLE FOR LYMPHADENOPATHY AND AUTOANTIBODY PRODUCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WHILE ISOFORM FASLS
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                      LQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLTIN--AASIPSGSHKVTLSSWY 165
                                                  LFHLQKE---LAE
                                                                           YFRAQMDPNRISEDSTHCFYRILRLHENADLQDSTLESEDTLPDSCRRMKQAFQGAVQKE 107
                                                                                                                               PHEGPLHPAPSAPAPAPP-----
                                                                                                                                                                      Similarity
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                                                                                                     -PPPSQPLPLPPLTPLKKKDHNTNLWLPVVFFMVLVALVGMGLG
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                                                                                                                                                        Conservative
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23.0%;
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                                                                                                                                                                                                                                  N-LINKED (GLCNAC. . .) (POTEN
N-LINKED (IN ISOFORM FASLS).
T -> A (IN STRAIN BALB/C).
E -> G (IN STRAIN BALB/C).
F -> L (IN GLD; ABOLISHES BIN
TO ITS RECEPTOR).
                                                    LREFTNOSLKVSSFEKQIANPST
                                                                                                                                                                      Score 177; DB 1
Pred. No. 4e-08;
                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL-ANCHOR EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC (FOTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
                                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                    PRO-RICH.
                                                                                                                                                                                                                                                                                                                                                                     POLY-PRO
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                                                                                                                                                                                                                          O ITS RECEPTOR).
37972E2728E0A1CA CRC64;
                                                                                                                                 -----PAASRSMFLALLGLGLGQVVCSIALFL 47
                                                                                                                                                           Mismatches
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                                                                                                                                                                                     279;
                                                                                                                                                                                                                                                    BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERALIZED
SIVE DISEASE
                                                                                                                                                            92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APOPTOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FASLS; ARE
                                                                                                        OAW-
                                                                                                                                                                                                                                                      OF)
                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                      FASL
    161
                                                                                                           101
                                                       134
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RESULT NASL_HMAN ID EASL_HMAN ID EASL_HMAN ID EASL_HMAN ACC P48023 DT 01-FEB DT 00X NCBIT RN 11-MT 1
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                                                                                                                                                            Matsumura M., Nakanishi Y., Ohba Y.;
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.

-I- FUNCTION: CYTOKINE THAT BINDS TO FAS ANTIGEN, A RECEPTOR THAT TRANSDICES THE APOPTOTIC SIGNAL INTO CELLS. MAY BE INVOLVED IN CYTOTOXIC T CELL MEDIATED APOPTOSIS AND IN T CELL DEVELOPMENT.

FAS-ANTIGEN MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED SUICIDE OF MATURE
                                                                                                                                                                                                                                                                                                                                                                                                     Wilkinson J.;
Submitted (MAY-1997) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-95071350; PubMed
Mita E., Hayashi N., Iio
Fusamoto H., Kamada T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schaetzlein C.E., Poehlmann R., Philippsen P., Eibel H. Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FASL_HUMAN P48023;
                                                                                                                                                                                                                                                                                                                                           TISSUE-Blood;
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-10 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. Schaetzlein C.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
FAS antigen ligand (Apoptosis antigen ligand)
TNFSF6 OR APTICGI OR FASL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-95127560; PubMed-7826947;
Takahashi T., Tanaka M., Inazawa J
"Human Fas ligand: gene structure,
specificity ".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               specificity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Fas ligand
lymphocytes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alderson M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Role of Fas ligand in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=95105731; PubMed=7528780;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                275
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                                                                                        T CELLS, OR BOTH.
SUBGUIT: HOMOTRIMER (PROBABLE).
SUBCELLULAR LOCATION: TYPE II M
SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY DATABASE: NAME-PROW; NOTE-CD guide CD178 entry;
                                                                    INTO THE EXTRACELLULAR FLUID,
                                                     SURFACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunol. 6:1567-1574(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GLYKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DTYGTALISGVKYKKGGLVINETGLYFVYSKVYFR-GQSCNNQPLNH---KVYM--RNSK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=7980502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Iio S., Takehara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     apoptosis induced by hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Commun.
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                                                            MEMBRANE PROTEIN. MAY BE I
PROBABLY BY CLEAVAGE FORM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Τ.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Suda T., Nagata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (APTL) (CD178 antigen)
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                                                                 BE RELEASED
FORM THE CELL
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Best Local
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EMBL; U08137; AAC50071.1; -.
EMBL; U11821; AAC50124.1; -.
EMBL; D38122; BAA07320.1; -.
EMBL; 296050; CAB09424.1; -.
EMBL; AB013303; BAA32542.1; -.
EMBL; AB013303; BAA32542.1; -.
EMBL; AB013303; BAA32542.1; -.
EMBL; AB013303; BAA32542.1; -.
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DOMAIN
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InterPro; IPR003636; TNF_abc.
InterPro; IPR003478; TNF_family.
Pfam; PF00229; TNF; 1.
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     274
                                                  283
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                                                  TYFGAFKV 290
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                                                                                                                                  SIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDA
                                                                                                                                                                                                              SWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVYVVKT
TFFGLYKL
                                                                                                                                                                                                                                                                                                                                                                                                                         LFLYFRAQMDPNRISEDSTHCFYRILRLHENADLQDSTLESEDTLPDSCRRMKQAFQGAV 104
                                                                                                  NSKY PQDLVMME:
                                                                                                                                                                                       EWEDTYGIVLLSGVKYKKGGLVINETGLYFVYSKVYFRGQSCNN---
                                                                                                                                                                                                                                                                                       EKQIGHPSPPPE---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 260
281 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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103
145
202
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                                                                                          -GKMMSYCTTGQMWARSSYLGAVFNLTSADHLYVNVSELSLVNFEESQ
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102
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21.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , WM
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N-LINKED (GLCNAC. . .) (PO'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 174; DB 1;
Pred. No. 7.4e-08;
3; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                  -----KKELRKVAHLTGKSNSRSMP-----L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           104;
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                                                                                          273
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TNF5_HUMAN
ID TNF5_HUMAN

STANDARD;

PRT;

261 AA

RESULT

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MEDLINE=93076854; Pu
Graf D., Korthaeuer
"Cloning of TRAP."
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01-APR-1993
01-APR-1993
16-OCT-2001
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with B
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01-APR-1993 (Rel. 25, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
CD40 ligand (CD40-L) (TNF-related activation
antigen GP39) (CD154 antigen).
TNFSF5 OR CD40LG OR CD40L OR TRAP.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae
                                                                                                                                                                                                                   regulation FEBS Lett. [6]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Braesch-Andersen
                                                                                                                                                                                                                                                                                                                                                                                                     Roberts R.L., Noelle R.J., Ledbetter J.A., Franck U., Och
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Gauchat J.F.M., Aubry
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Macduff B.M.,
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MEDLINE=93094757; PubMed=1281209;
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Nonoyama S., Bajorath J., Grosmaire L.S., Stenkamp
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Karpsusas M., Hsu
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                                                     MEDLINE=98266353;
                                                                                                          "2-A crystal
                                                                 3D-STRUCTURE
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Grosmaire L.S., Kullas C.D., C
n S., Noelle R.J., Stamenkovic
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Y.-M., Wang J.-
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VARIANTS
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Copeland N.G., Bedell M.A., Edelhoff S.,
Simoneaux D.K., Fanslow W.C., Belmont J.
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Lin Q., Rohrer J., Allen R.C., Larche Gatti R.A., Derauf D.C., Belmont J.W.,
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Giliani S., Mantuano E., Fasth A., Andersson
Cavagni G., Reznick I., Levy J., Zan-Bar I.,
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MEDLINE=93156839; PubMed=7679206;
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IgM syndrome.";
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"CD40 ligand mutations i
Nature 361:541-543(1993)
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Disanto J.P., Bon
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MEDLINE=97295077; PubMe
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                                                                                                                                                                                                                                                                                                                                                                                                            "A single strand conformation polymorphism study of CD40 ligand Efficient mutation analysis and carrier detection for X-linked light syndrome.":
         DISPASE: DEFECTS IN THESES ARE THE CAUSE OF AN X-LINKED IMMUNODEFICIENCY WITH HYPER-IGM (HIGM!), AN IMMUNOGLOBULIN ISOTYPE SWITCH DEFECT CHARACTERIZED BY ELEVATED CONCENTRATIONS OF SERUM IGM AND DECREASED AMOUNTS OF ALL OTHER ISOTYPES. AFFECTED MALES PRESENT AT AN EARLY AGE (USUALLY WITHIN THE FIRST YEAR OF LIFE) RECURRENT BACTERIAL AND OPPORTUNISTIC INFECTIONS, INCLUDING RECURRENT BACTERIAL AND OPPORTUNISTIC INFECTIONS, INCLUDING PNEUMOCYSTIS CARINII PNEUMONIA AND INTRACTABLE DIARRHEA DUE TO CRYPTOSPORIDIUM INFECTION. DESPITE SUBSTITUTION TREATMENT WITH INTRAVENOUS IMMUNOGLOBULIN, THE OVERALL PROGNOSIS IS RATHER POOR, SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY. DATABASE: NAME=CD40LDase;
                                                                                                                                                                                                                                              . Genet. 99:624-62/(1997). FUNCTION: MEDIATES B-CELL PROLIFERATION IN THE PRESENCE STIMULUS AS WELL AS IGE PRODUCTION IN THE PRESENCE INVOLVED IN IMMUNOGLOBULIN CLASS SWITCHING.
                                                                                                                                                                                        SUBUNIT: HOMOTRIMER.
SUBCELLULAR LOCATION: TYPE
EXTRACELLULAR SOLUBLE FORM.
TISSUE SPECIFICITY: SPECIFI
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PROSITE; PS50049; TNF_2; 1.

Cytokine; Transmembrane; Glycoprotein; Signal-anchor;
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FTP-"ftp://ftp.expasy.org/databases/cd40lbase".
DATABASE: NAME-PROW; NOTE-CD guide CDL54 entry;
WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cdl54.htm".
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$26694;
$28017;
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                                                         ENSF -- EMOKGDONPOIAAHV ----- ISEASSKTTSVLQWAEKGYYTMSNNLVTLENGK
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JOINED.
JOINED.
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                                                                                                                                                                                                                                                       Score 169.5;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                   SE -> RG (IN H1GM1).

/FTId=VAR_007516.

W -> C (IN H1GM1).
                                                                                                                                                                                                                                                                                                                                                                                                         M -> R (IN H1GM1).
/FTId=VAR_007513.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                             /FTId-VAR_007515
                                                                                                                                                                                                                                                                                                                                                                           A -> E (IN H1GM1).
/FTId=VAR_007514.
                                                                                                                                                                                                                                                                                                                                                                                                                                        N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ymorphism.
                                                                                                                                                                                                                                                                                                                                                           -> A (IN H1GM1).
                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                 C (IN H1GM1).
                                                                                                                                                                                                                                                                                                                                                                                                                                        (GLCNAC.
 ----FIASLCLKSPGRFERILLRAANT
                                                                                                                                                                                                                                                         5; DB 1;
l.6e-07;
                                                                                                                                                                                                                                         116;
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                                                                                                                                                                                                                                            Query Match
Best Local
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097605;
16-0CT-2001
16-0CT-2001
16-0CT-2001
                                                                                                                                                                                                                                                                                                                           DOMAIN
DISULFID
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a copyright in the EMBL between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CD40 ligand (CD154 antigen).
TNFSF5 OR CD40LG OR CD40L.
Felis silvestris catus (Cat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ProDom; PD008600; TNF_5; 1. SMART; SM00207; TNF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003263; TNF_5
InterPro; IPR000478; TNF_fe
Pfam; PF00229; TNF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF07910; HSSP; P29965;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00251; TNF_1; PROSITE; PS50049; TNF_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cytokine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Thymus
         126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      239 KNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         212 H--SSAKPCGQQSIHLGGVFELQPGASVFVNVTDPSQVSHGTGFTSFGLLKL
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                                                                                                                                                                    11 APSAPAPAPPPAASRSMFLALLGLGLGQVVCSIALF-LYFRAQM----DPNRISEDSTHC
                                                                                                                                                                                                                                          Local
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GSWLDVAQRGKPEAQPFAHLTINAASIPSGSHKVTLSSWYHDRGWAKISN--MTLSNGK-
                                                                                                                              APRSVAPGPP--VSMKIFMYLLTVFLITQMIGSALFAVYLHRRLDKIEDERNLYED--FV
                                          FMKTLQKCNKGEGALSLL-----NCEEIKSRFE-AFLKEIMLNKETKKEKNV----
                                                                                   FYRILRLHENADLQDSTLESEDTLPDSCRRMKQAFQGAVQKELQHIVGPQRFSGAPAMME 125
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                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transmembrane;
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(Rel. 40, Last annotation
(CD154 antigen).
                                                                                                                                                                                                                      Conservative
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177
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217
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28727
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46
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                                                                                                                                                                                                                 50;
                                                                                                                                                                                                                                        Score 167; DB 1;
Pred. No. 2.7e-07;
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349FA0391FB7B932 CRC64;
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                                                                                                                                                                                                                 117;
                                                                                                                                                                                                                                                       Length 260;
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RESULT 11
TNFA_CAVPO
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                                                                                          EMBL; U39839;
EMBL; U77036;
HSSP; P06804;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=DUNKIN-HARTLEY;
MEDLINE=97462215; PubMed=9316485;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-HARTLEY; TISSUE-Lung;
Yuan H.T., Kelly F.J., Bingle C.D.;
Submitted (NOV-1995) to the EMBL/Ge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TNFA_CAVPO
            ProDom; PD002012; TNF_abc; SMART; SM00207; TNF; 1.
                                                                                                                                                or send an
                                                                                                                                                                                         use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10141;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tumor necrosis
PROSITE;
                                                     Pfam; PF00229; TNF; 1
                                                                                                                                                              entities
                                                                                                                                                                           modified
                                                                                                                                                                                                                                 This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     factor-alpha.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   White A.M., Yoshimura T., Smith "Airway inflammation induced by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       THE OR THEA
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                                     PRINTS; PR01234; TNECROSISECT.
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                                                                  [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240
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                                                                              nterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -OCT-1996
                                                                                                                                                                                                                                                                               SUBUNIT: HOMOTRIMER (BY SIMILARITY).
SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN.
SUBCELLULAR SOLUBLE FORM (BY SIMILARITY).
PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE
PROTEDITIC PROCESSING (BY SIMILARITY).
DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEA
CANCER AND INFECTION, AND IS CHARACTERIZED BY GE
                                                                                                                                                                                                                                                                                                                                                                                                     J. Physiol. 273:L524-L530(1997).

FUNCTION: TWE IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKINE WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF CACHEXIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE
                                                                                                                                                                                                    European
                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
                                                                                                                                                                                                                                                                       AND
                                                                                                                                                                                                                                                                                                                                                                               CONDITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LRVNQDGFYYLVANICF-RHHETSGSVPTDYLQLMVYVVKTSIKIPSSHN--LMKGGSTK
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                                                                  IPR000478;
                                                                              IPR003636; TNF_abc
                                                                                                                                                equires a license agreement (Semail to license@isb-sib.ch).
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(Rel.
                                                                                                                                                                        Bioinformatics Institute. The profit institutions as long this statement is not removed.
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                                                                                                         AAB19210.1; -.
                                                                                                                       AAB06492.1;
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39,
                                                                TNF_family.
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Last annotation update)
precursor (TNF-alpha) (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     recombinant
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                                                                                                                                                                                                                              It is produced through a collaboration
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pinant guinea
                                                                                                                                                              (See http://www.isb-sib.ch/announce/
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BY GENERA
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                                                                                                                                                                                                                    EMBL outstation
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Best Local
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16-OCT-2001
CD40 ligand.
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SEQUENCE
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                    ProDom; PD008600; TNF_5
SMART; SM00207; TNF; 1.
                                                                           EMBL; AF086711; AAD04375.1; HSSP; P29965; 1ALY.
                                                                                                             entities requires a or send an email to
                                                                                                                                     modified and
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                                                                                                                                                           the
                                                                                                                                                                                                                                                                                    Submitted
                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; (
Mammalia; Eutheria; Carnivora;
                                                                                                                                                                                                                                                                                                                                                                               Canis familiaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                 097626;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TNF5
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                                            Pfam; PF00229;
                                                   InterPro; IPR003263; TNF_5.
InterPro; IPR000478; TNF_family.
                                                                                                                                                                        between
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                                                                                                                                                                                                                                                                                                 "Adjuvant
                                                                                                                                                                                                                                                                                                            Hosie M.H
                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                       16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55
                                                                                                                                                           ween the
European
                                                                                                                                                                                                                                    ie M.H., Willett B.J.;
juvant properties of canine CD40L.";
juvant properties of canine CD40L.";
juvant properties of canine CD40L.";
mitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
FUNCTION: MEDIATES B-CELL PROLIFERATION IN THE PRESENCE OF I.
STIMULUS AS WELL AS IGE PRODUCTION IN THE PRESENCE OF I.
INVOLVED IN IMMUNOGLOBULIN CLASS SWITCHING (BY SIMILARITY).
SUBUNIT: HOMOTRIMER (BY SIMILARITY).
                                                                                                                                                                                                     SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS EXTRACELLULAR SOLUBLE FORM (BY SIMILARITY).
SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CANFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QKGDRLSAEVNLPQYLDFADSGQIYFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RAGEEISIQVSNPSLLD-PDQDATYFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGSHKVTLSSWYHDRGWAKISN-MTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VIGPQREEQFSSGPPF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LQLMVYVVKTSIKIPSSHNLM-------KGGSTKNWSGNSEFHFYSINVGGFFKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLLTHTVSRLAVSYPEKVNLLSAIKSPCQKETPEGAERKPW
                                                                                                                                                                                                                                                                                                                                                                                           OR.
                                                                                                               an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  non-profit institu
                                                                                                                                                                                                                                                                                                                                                                                           CD40LG
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(Rel.
(Rel.
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80
36
147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -LQWLSKRANALLANGMGLSDNQLVVPSDGLYLIYSQVLFK----
                                                                                                                                                            Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                        N.A
                                            TNF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                          OR CD40L.
                                                                                                                                                                                                                                                                                                                                                                               (Dog).
                                                                                                                                                                                                                                                                                                                                                                                                                            40,
40,
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                                TNF_5; 1.
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234
56
178
                                                                                                                           license
                                                                                                                                                                                                                                                                                                                                                                    Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25793
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                                                                                                                                                 institutions as long
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Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26;
                                                                                                                           agreement
                                                                                                                                      is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TUMOR NECROSIS FACTOR.
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
BY SIMILARITY.
; 7272C940393E7E9B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 157;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                          Fissipedia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            286
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                                                                                                                           (See
                                                                                                                                                 There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; 1
1.7e-06;
nes 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Å
                                                                                                                                                                                                                                                                                                                                                           Canidae; Canis
                                                                                                                           http://www.isb-sib.
                                                                                                                                      Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
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                                                                                                                                                            restrictions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -GQGCPSY
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                                                                                                                                         for
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PROSITE;

PS50049; PS00251;

TNF_1; TNF_2;

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Best Local S
Matches 75
                                                                                                                                                                                                                                                                                                                   01-AUG-1992
16-OCT-2001
16-OCT-2001
CD40 ligand
GP39)
3D-STRUCTURE MODELING OF 115-260. MEDLINE-93200072; PubMed-8095800; Peitsch M.C., Jongeneel C.V.;
                                   Nature
[4]
                                           Farrah T., Smith C.A.; "Emerging cytokine family."; Nature 358:26-26(1992).
                                                                          SIMILARITY TO THE THE FAMILY MEDLINE-92310561; Pubmed-137
                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-92244364; PubMed-1374165;
Armitage R., Fanslow W., Sato T.A.,
Arduff B.M., Anderson D.M., Gimpel
Maliszewski C.R., Clark E.A., Smith
Spriggs M.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
DISULFID
CARBOHYD
SEQUENCE
                                                                                                         Submitted (APR-2001)
                                                                                                                      Spriggs M.K.;
                                                                                                                                 REVISION TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cytokine;
DOMAIN
                                                                                                                                                    Nature 357:80-82(1992)
                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                       TNESES OR CD40LG OR CD40L.
                                                                                                                                                                                                                                                                                                                                                                                               MOUSE
                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                    INF5_MOUSE
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                                                                                                                                                                         ecular and biological
                                                                                                                                                                                                                                                                                                                                                                                                                                    GSSKPCGQQ-----SIHLGGVFELHPGASVFVNVTDPSQVSHGTGFTSFGLLKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NWS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GSWLDVAQRGKPEAQPFAHLTINAASIPSGSHKVTLSSWYHDRGWAKISN--MTLSNGK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APSAPAPAPPPAASRSMELALLGLGGLGQVVCSIALE-LYERAQM----DPNRISEDSTHC 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LAVKROGLYYVYAQVTFCSNRAASSQAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LRVNQDGFYYLYANICF-RHHETSGSVPTDYLQLMVYVVKTSIKIPSSHN--LMKGGSTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------QKGDQDPRIAAHVISEASSNPA----SVLRW-APKGYYTISSNLVSLENGKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FMKTLQKCNKGEGSLSLL------NCEEIKSQFE-AFLKEIM-LNNEMKKEENIAM--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FYRILRLHENADLODSTLESEDTLPDSCRRMKQAFQGAVQKELQHIVGPQRFSGAPAMME 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transmembrane;
1 22
23 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                         -GNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKV
                                                                                                                              198.
                                                                                                                                                                                                                                                                                                                            (Rel. 23, Created)
(Rel. 40, Last sequence update)
(Rel. 40, Last annotation updat.)
(TNF-related activation protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               260 /
                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                À
                                                                           PubMed-1377364;
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217
239
28688
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                                                                                                         the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glycoprotein; Signal-anchor.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                         characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 157; DB 1
Pred. No. 2e-06;
D; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
N-LINKED (GLCNAC. . .) (POTENTIAL)
, 604F69A19E98EB70 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                      Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIGNAL-ANCHOR
                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                          Clifford K.N., Strock
S.D., Davis-Smith T.,
C.A., Grabstein K.H.,
                                                                                                                                                                                                                                                                                                                           protein) (TRAP)
                                                                                                                                                                                                                                                                                                                                                                                  260
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                                                                                                         databases
                                                                                                                                                                       ø
                                                                                                                                                                       murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 260;
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                                                                                                                                                                                                                  Strockbine
                                                                                                                                                                                                                                                                     Euteleostomi;
; Murinae; Mus
                                                                                                                                                                                                                                                                                                                            (i
                                                                                                                                                                       ligand
                                                                                                                                                                                                                                                                                                                            cell antigen
                                                                                                                                                                                           Cosman
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RESULT 14
TNFA_HORSE
ID TNFA_H
AC P29553
DT 01-APR
DT 01-APR
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00251; TNF_1; 1
PROSITE; PS50049; TNF_2; 1
Cytokine; Transmembrane; G
DOMAIN
TRANSMEM
23
46
TNFA_HORSE
P29553;
01-APR-1993
01-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   between the Swiss Institute of Bioinformat
the European Bioinformatics Institute. The
use by non-profit institutions as long
modified and this statement is not removed.
entities requires a license agreement (See
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ProDom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGD; MGI:88337; Tnfsf5.
InterPro; IPR003263; TNF_5.
InterPro; IPR000478; TNF_family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "A 3-D model for the CD40 ligand predicts that it is a co
similar to the tumor necrosis factors.";
Int. Immunol. 5:233-238(1993).
-!- FUNCTION: MEDIATES B-CELL PROLIFERATION IN THE ABSENC
STIMULUS AS WELL AS IGE PRODUCTION IN THE PRESENCE OF
INVOLVED IN IMMUNOGLOBULIN CLASS SWITCHING.
-!- SUBUNIT: HOMOTRIMER.
-!- SUBUNIT: HOMOTRIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00229;
                                                                                                                      206
                                                                                                                                                 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE SPECIFICITY:
                                                                                                                                         KGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKV
                                                                                                                                                                                                                                                                                                                                                                                  PAPSAPAPAPPPAASRSMFLALLGLGL-GQVVCSIALFLYFRAQMDPNRISEDSTHCFYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X65453; CAA46448.2;
S21738; S21738.
1CDA; 31-OCT-93.
                                                                                                                                                                                            SNGK-LRVNQDGEYYLYANICF-RHHETSGSVPTDYLQLMVYVVKTSIKIPSSHN---LM
                                                                                                                                                                                                                                    --EKKENSF--EMQRGDEDPQIAAHVVSEA-----NSNAASVLQWAKKGYYTMKSNLVML 154
                                                                                                                                                                                                                                                              APAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHKVTLSSWYHDRGWAKISNMT-L 178
                                                                                                                                                                                                                                                                                             -VNLHEDFVFIKKLKRCNKGEGSLSLLNCEEMRRQFEDLVKDITLNKE------
                                                                                                                  KAANTHSSSQLCEQO--SVHLGGVFELQAGASVFVNVTEASQVIHRVGFSSFGLLKL
                                                                                                                                                                            ENGKQLTVKREGLYYVYTQVTFCSNREPSSQRP
                                                                                                                                                                                                                                                                                                                         ILRLHEN----ADLQDSTLESEDTLPDSCRRMKQAFQGAVQ-----KELQHIVGPQRFSG 119
                                                                                                                                                                                                                                                                                                                                                          PSPRSVATGLP--ASMKIFMYLLTVFLITQMIGSVLFAVYLHRRLD--KVEEE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LYMPHOCYTES
                                                                                                                                                                                                                                                                                                                                                                                                                        74;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PD008600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47
177
239
260
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                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TNF;
                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TNF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TNF_5; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               260 F
217 F
239 P
29370 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                      9.88;
24.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPECIFICALLY EXPRESSED
                                                                                                                                                                                                                                                                                                                                                                                                                      53;
                                                                                                                                                                                                                                                                                                                                                                                                                   Score 153; DB
Pred. No. 4.4e
53; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-LINKED (GLCNAC. . .) (POTENTIAL).
; 7E1AC117473672AD CRC64;
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                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TUMOR NECROSIS FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                   153; DB
No. 4.4e-
                                          234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 moved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             There are no rest
                                          Ã
                                                                                                                                                                                                                                                                                                                                                                                                                      110;
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Best Local Similarity
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Gene 107:319-321(1991).

Gene 107:319-321(1991).

-I FUNCTION: THE IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKINE FUNCTION: THE INDUCTION OF EUROPHAIN TUMOR CELL LINES, IT IS AWPLICATED IN THE INDUCTION OF CACHEXIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION OR BY STIMULATION OF INTERLEURIN 1 SECRETION, IT CAN STIMULATE OR BY STIMULATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Equus caballus (Horse).
Eukaryota; Metazoa; Chordata; Craniata; Verto
Eukaryota; Metazoa; Perissodactyla; Equidae;
Mammalia; Eutheria; Perissodactyla; Equidae;
MCBI_TaxID-9796;
                                                                                                                                                                                                                                                                                                                                   DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR01234; TNECROSISFCT ProDom; PD002012; TNF_abc; 1. SMART; SM00207; TNF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=92084125; PubMed=1748301;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TNF OR TNFA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tumor necrosis factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUL-1999 (Rel. 38,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROTEOLYTIC PROCESSING.
-1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Cloning and characterization of gene TNF alpha encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00251; TNF_1; 1. PROSITE; PS50049; TNF_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00229; TNF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M64087; AAA30959.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR003636; TNF_abc
InterPro; IPR000478; TNF_fam.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P01375; 4TSV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an
                                                                                                                                                                                                                                                                                                                                                                                                     PROPEP
                                                                                                                                                                                                                                                                                                                                                                    TRANSMEM
                                                163
                                                                                 225
                                                                                                                  107
                                                                                                                                                 166
                                                                                                                                                                                                                 111 IVGPQRFSGAPAMMEGSWLDVAQRGK-----PEAQPFAHLTINAASIPSGSHKVTLSSWY 165
                                                                                                                                                                                  55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: EXTRACELLULAR SOLUBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBUNIT: HOMOTRIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONDITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JQ1344; JQ1344.
                                                                                                                GRANALLANGVKLTDNQLVVPLDGLYLIYSQVLFK--
                                                                                                                                                                                VIGPQREEQLPNAFQ-SINPLAQTLRSSSRTPSDKPVAHVVAN----PQAEGQL---QWL
               PSLLD-PDQDATYFG
                                                SYPSKVNLLSAIKSPCHTESPEQAEAKPW---
                                                                                 KIPSSHNLMKG----
                                                                                                                                                 HDRGWAKISN-MTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVYVVKTSI
--
                                                                                                                                                                                                                                                                                                                                  Cytotoxin; Transmembrane; Glycoprotein; Signal-anchor.

1 77 BY SIMILARITY.

78 24 TUMOR NECROSIS FACTOR.

36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).

146 178 BY SIMILARITY.

234 AA; 25469 MW; E79ACE91143DF373 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   email to license@isb-sib.ch).
                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TNF_family.
                                                                                                                                                                                                                                                                   9.5%;
24.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  precursor (TNF-alpha) (Cachectin)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE II MEMBRANE PROTEIN. ALSO FORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R.A.;
                                                                                                                                                                                                                                                    38;
                                                                                 -GSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSN
                                                                                                                                                                                                                                                                     Score 149; DB 1;
Pred. No. 8.5e-06;
                                                                                                                                                                                                                                                     Mismatches
                                                   -YEPIYLGGVFQLEKGDQLSAEINQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Equus
                                                                                                                    -GQGCPSTHVLLTHTISRLAV
                                                                                                                                                                                                                                                                                     Length 234;
                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                       38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AS
                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                      224
                                                                                      272
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RESULT 15
TNFA_MACFA
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Qy
                           Query Match
Best Local S
Matches 50
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P79337;
15-JUL-1998
15-JUL-1998
15-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.

-I- FUNCTION: THE IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKINE WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF CACHEXLA, IT IS A POTENT BYROGEN CAUSING FEVER BY DIRECT ACTION OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN
                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tatsumi M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cercopithecinae; Macaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Macaca fascicularis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      THE OR THEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tumor necrosis
                                                                                                                                                                                                                                                                                                                                 entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ++
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Lymphocytes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                SEQUENCE
                                                                                                                                                                    proSITE; PS00251; TNF_1; 1.
proSITE; PS50049; TNF_2; 1.
Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Signal-anchor
                                                                                                                                                                                                             PRINTS; PR01234; TNECROSISFCT ProDom; PD002012; TNF_abc; 1. SMART; SM00207; TNF; 1.
                                                                                                                                                                                                                                                       Interpro; IPR003636; TNF_abc
Interpro; IPR000478; TNF_fam.
pfam; pF00229; TNF; 1.
                                                                                                                                                                                                                                                                                             EMBL; AB000513; BAA19131.1; -. HSSP; P01375; 4TSV.
                                                                                                                                                                                                                                                                                                                                                                    modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        +
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                                                                                                                DISULFID
                                                                                                                              TRANSMEM
                                                                                                                                           CHAIN
                                                                                                                                                        PROPEP
111 IVGPOR--FSGAPAMMEGSWLDVAQRGK---PEAQPFAHLTINAASIPSGSHKVTLSSWY 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: HOMOTRIMER.
SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS
EXTRACELLULAR SOLUBLE FORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM PROTEOLYTIC PROCESSING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF CANCER AND INFECTION, AND IS CHARACTERIZED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONDITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CANCER AND INFECTION,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AND MALNUTRITION
                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Metazoa;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Rel.
                                                                                                  233 AA;
                             Conservative
                                                                                                                145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  factor precursor (TNF-alpha)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36, Created)
36, Last sequence up
38, Last annotation
                                                                                                                76
233
56
177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Crab eating macaque) (Cynomolgus monkey).
Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           230
                                                                                                     25558
                                           9.5%;
                                                                                                                                                                                                                                                                      TNF_family.
                                                                                                     WW;
                                 38;
                              Score 148.5; DB 1
Pred. No. 9.3e-06;
8; Mismatches 68
                                                                                                               BY SIMILARITY.
TUMOR NECROSIS FACTOR.
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                     6ABF2C3AB132C217 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA
                                                             DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Cachectin)
                                                                                                                                                                                                                                                                                                                                                                        Usage by
                                 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISEASES,
BY GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL
                                                          Length
                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ILL
                                                                                                                                                                                                                                                                                                                                                                                                                    a collaboration -
MBL outstation -
                                   39;
                                                                                                                                                                                                                                                                                                                                                                          for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HEALTH
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                                 Gaps
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55 VIGPOREEFPKDPSLI--SPLAQAVRSSSRTPSDKPVAHVVAN----PQAEGQL---QWL 105

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein - protein search, using sw model
                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
   1525.5
1492
1496
1426
1227
1027
205.2
263.5
218.5
218.5
180.5
179
179
179
179
174.5
174.5
                                                                                                                                                                                        Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq length:
seq length:
                                                                                                                                                                                                                                                                                                                                                                                                                   SPTREMBL_19:*
1: sp_archea:*
2: sp_bacteria
3: sp_fung1:*
4: sp_human:*
5: sp_inverteb
                                                                                                                                                                                       Query
Match
                                                                                                                                                                                                                                                                                        6:
7:
9:
110:
112:
113:
115:
     97.7
95.6
91.4
91.4
78.6
778.6
778.6
117.4
117.4
111.5
111.5
111.5
111.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
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1561
1 GVPHEGPLHPAPSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          562222 seqs, 172994929 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                July 8,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GVPHEGPLHPAPSAPAPAPP.....LLDPDQDATYFGAFKVQDID
                                                                                                                                                                                                                                                                                                                                                                         sp_phage: *
                                                                                                                                                                                                                                                                                                                                                                                    sp_organelle:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                   sp_archea:*
sp_bacteria:*
                                                                                                                                                                                                                                                                                                                                                                                               sp_mhc:*
                                                                                                                                                                                                                                                                                                                                                                                                         sp_mammal:*
                                                                                                                                                                                                                                                                                                                                                                                                                    sp_invertebrate:*
                                                                                                                                                                                                                                                                                                         sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
                                                                                                                                                                                                                                                                                     sp_bacteriap:*
sp_archeap:*
                                                                                                                                                                                                                                                                                                                                          sp_virus:*
                                                                                                                                                                                                                                                                                                                                                   sp_rodent:*
                                                                                                                                                                                                                                                                                                                                                               sp_plant:*
                                                                                                                                                                                        Length
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Q9rly0 mus musculu
Q9ese2 rattus norv
Q9jlk9 mus musculu
Q96q17 homo sapien
Q9jjk8 mus musculu
Q91zl9 rattus norv
Q9ddz5 brachydanio
Q90wt9 gallus gall
Q9bdn3 actus trivi
Q9bdn3 actus trivi
Q9md3 actus trivi
Q9md5 macaca neme
Q9bdm5 macaca nula
Q95n10 sus scrofa
Q918d8 gallus gall
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ALIGNMENTS

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OT Ol-MAY-2000 (TREMBLEEL. 13, Created)
DT Ol-MAY-2000 (TREMBLEEL. 13, Last sequence update)
DT Ol-MAY-2000 (TREMBLEEL. 19, Last annotation update)
DT Ol-DEC-2001 (TREMBLEEL. 19, Last annotation update)
OSTEOCLAST DIFFERENTIATION FACTOR.

GN THESTIL.

OS MUS musculus (Mouse).

OC ELKATYOCIS (Mouse).

OC ELKATYOCIS (Mouse).

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TAXID=10090;

RN STOUBNCE FROM N.A.

STRAIN=129;

RN STOUBNCE FROM N.A.

STRAIN=129;

RN STOUBNCE FROM N.A.

RA KOdaira K., Kodaira K., Mizuno A., Yasuda H., Shima N., Murakami A.,

RA KOdaira K., Kodaira K., Mizuno A., Yasuda H., Shima N., Murakami A.,

RA Veda M., Higashio K.;

RT Toloning and characterization of the gene encoding mouse osteoclast

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RP EMBL; AB02203; BAA36970.1; JOINED.

DR HSSP; P5051; LDOG.

DR HSSP; P50521; LDOG.

DR HSSP; P50521; LDOG.

DR FINE; IDOG.

DR PFO0229; TNF; I.

DR PROSITE; PS50049; TNF; I.
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Query Match Best Local Similarity

97.7%; 98.6%;

Score 1525.5; DB 11; Pred. No. 1.5e-132;

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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
NCBI_TaxID=10116;
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MEDLINE-20540945; PubMed-11092398;
Xu J.K., Tan J., Huang L., Gao X.H.,
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Pfam; PF00229; TNF; 1.
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                                            GAPAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHKVTLSSWYHDRGWAKISNMTL
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MGD; MGI:1100089; Tnfsf11.

InterPro; IPR003263; TNF_5.

InterPro; IPR003636; TNF_family.

InterPro; IPR003636; TNF_family.

InterPro; IPR000478; TNF_family.

Pfam; pF00229; TNF; 1.

ProDom; pD002102; TNF_5; 1.

SMART; SM00207; TNF; 5.

PROSITE; pS50049; TNF_2; 1.

SEQUENCE 287 AA; 32234 MW; 8B5
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EMBL; AB032771; BAA97257.1; -.
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Metazoa; Chordata; C.
Metazoa; Rodentia; S.
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and Their Differential Expression in F
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Best Loc
Matches
                MGD; MGI:1100089; Tnfsf11.
InterPro; IPR003263; TNF_5.
InterPro; IPR003636; TNF_abc.
InterPro; IPR003636; TNF_family.
Pfam; PF00229; TNF; 1.
ProDom; PD002012; TNF_abc; 1.
ProDom; PD008600; TNF_5; 1.
SMARP; SM00207; TNF; 1.
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Q9JJK8;
Q9JJK8;
Q1-QCT-2000 (TrEMBLrel. 15, C:
01-QCT-2000 (TrEMBLrel. 15, L:
01-DEC-2001 (TrEMBLrel. 19, L:
RECEPTOR ACTIVATOR OF NF-KB L
                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted
EMBL; AB06
SEQUENCE
                                                                                                             Endocrinology 142:1419-1426(2001).
EMBL; AB032772; BAA97258.1; -
                                                                                                                                                 MEDLINE-21150053; PubMed-11250921
Ikeda T., Kasai M., Utsuyama M.,
"Determination of Three Isoforms
                                                                                                                                         Factor-kappaB Ligand
                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                             TNFSF11 OR RANKL 3.
                                                                                                   HSSP; P50591; 1D0G.
                                                                                                                                                                                                      NCBI_TaxID=10090;
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"Human RANKL 150form.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ
EMBL; AB061227; BAB71768.1; •.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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Mammalia; Eutheria;
NCBI_TaxID=9606;
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Homo sapiens (Human
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Local Similarity
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         PS50049; TNF_2; 1.
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                                                                                                                                                                     PubMed=11250921;
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Primates;
 22150 MW;
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Pred.
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Sciurognathi;
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                                                                                                                                        ., Hirokawa K.;
ms of the Receptor Activator
Differential Expression in F
401C13EB5E8CE166 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5C7754CE32E6F368 CRC64;
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No. 4.1e-105;
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thi; Muridae;
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; Murinae; Mus
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Best Local S
Matches 199
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Q9DDZ5;
Q1-MAR-2001 (TrEMBLI
01-MAR-2001 (TrEMBLI
01-DEC-2001 (TrEMBLI
TRAIL-LIKE PROTEIN
TNESF10L.
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O91ZI9;
01-DEC-2001 (TrEMBLr
01-DEC-2001 (TrEMBLr
01-DEC-2001 (TREMBLR
TNESF11 (FRAGMENT).
TNESF11,
Rattus norvegicus (R
                                   Actinopterygii; Neopterygi
Cypriniformes; Cyprinidae;
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-F344;
Odgren P.R., Kim N., van Wesenbeeck L., MacKay C.A., Mass Safadi F.F., Popoff S.N., Lengner C., van Hul W., Chol Y Safadi F.F., Popoff S.N., Lengner C., van Hul W., Chol Y Evidence that the rat osteopetrotic mutation toothless the Tnfsfll (TRANCE, RANKL, ODF, OPGL) gene.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF425669; AAL23963.1; -.

NON_TER 1
1
SEQUENCE 53 AA; 5876 MW; 8A71E32F2B6A9410 CRC64;
  SEQUENCE
                                                                                                    Eukaryota; Metazoa;
                                                                                                                      Brachydanio rerio (Zebrafish)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                       242
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llarity 100.0%;
Conservative (
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                                                        io (Zebrafish) (Zebra dar
zoa; Chordata; Craniata;
    Neopterygii; Teleostei;
Cyprinidae; Danio.
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96.2%;
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Pred. No. 5.5e-18;
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Pred. No. 1.3e-89;
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Sciurognathi; Muridae;
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                                                                                            Vertebrata; Euteleostom1;
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W., Choi Y., Marks
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Comp.

ds in the fish ovary.";
Biochem. Physiol. B, Comp.
AF250041; AAG47640.1; ...
P50591; 1D0G.

Bobe J., Goetz F.W.;

"Molecular cloning and expression of a TNF receptor and two ligands in the fish ovary.";

Biochem. 129:475-481(2001).

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Goetz F.W.;

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InterPro; IPR003263; TNE_5.
InterPro; IPR003636; TNE_family.
InterPro; IPR003478; TNE_family.
Pfam; PF00229; TNE; 1.
ProDom; PD002012; TNF_5: 1.
ProDom; PD008600; TNE_5: 1.
SMART; SM00207; TNE; 1.
PROSITE; PS50049; TNF_2; 1.
SEQUENCE 214 AA; 24093 MW; 980
                                                                                                                                                                                                                    Query Match
Best Local S
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Q90WT9;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
TNF-RELATED APOPTOSIS INDUCING LIGAND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                                                  Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases EMBL; AY057941; AAL23702.1; -. SEQUENCE 287 AA; 32092 MW; DB06E1C95087B108 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                             ovary
                                                                                                                                                                                                                                                                                                                                                                                                    "TNF-related apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               148
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  105
                                              119
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                                                                                                 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RMKQAFQGAVQKELQHIVGPQRFSGAPAMME-----GS--WLDVAQRGKPEAQPFAHLTI 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YANICFRHHETSGSVPTDYLQLMVYVV--KTSIKIPSSHNLMKGGSTKNWSGNSEFHFYS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKV 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : || |:||||:|: : ||:|::: : ::|||||:::
VYQGGLFELRAGDEVFVSVSSPTMVYGEDSSSYFGAFRL 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YSQVYFRYPSPSDSDQSSVSHQLVQCIYKKTSYLNPI--QLLKGVGTKCWAPDAEYALHS
                                                                                                                                          SEDSTHCFYRILRLHENADLQDSTLESEDTLPDSCRRMKQAFQGAVQKELQHIVGPQRFS
                                                                                              SSEELRCLQLINQQQEGSNLEE---LISN----QSCLKLANTIKAYVATVTENVISRSVVN
                                              GAPAMMEGSWLDVAQ----RGKPEAQPFAHLTI----NAASIPSG--
  EA---
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69; Conserv
                                                                                                                                                                                                                         Similarity
-QKSYFNISEGQVATKTLGKPSAHLIFRPQNPAQDGSSRRFGNLSQSCRHAITRW
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inducing ligand
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pred. No. 2.3e-16;
2; Mismatches 77;
                                                                                                                                                                                               Score 218.5; DB 13
Pred. No. 4.8e-12;
2; Mismatches 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98C002474FF691AA CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                         (TRAIL) expression
                                                                                                                                                                                                                                                   DB 13;
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                                                          SHKVTLSSW
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RESULT Q9BDM3

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RESULT
Q9BDN3
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                      20
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Best Local Similarity
Matches 77; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=21383618; PubMed=11491535;
Villinger F., Bostik P., Mayne A.E.,
Weiss W.R., Ansari A.A.;
Weiss W.R., Ansari A.A.;
"Cloning, sequencing, and homology &
"Cloning, sequencing, and homology &
ras/Fas-11gand and co-stimulatory mc
Immunogenetics 53:315-328(2001).
EMBL, AF344844; AAK37603.1; ".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Callithrix jacchus (Common marmoset).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9BDN3;
01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9BDN3
                                                                                                                                                                                                                                                                                                                  PROSITE; PS00251; TNF_1; 1.
PROSITE; PS50049; TNF_2; 1.
SEQUENCE 261 AA; 29360 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CD154 PROTEIN
                                                                                                                                                                                                                                                                                                                                                        HSSP; P29965; 1ALY.
InterPro; IPR003263; TNF_5.
InterPro; IPR003278; TNF_family.
Pfam; PF00229; TNF; 1.
ProDom; PD008600; TNF_5; 1.
SMART; SM00207; TNF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9483;
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                                                                                                                                                                                                                     PAPSAPAPAPPPAASRSMELALLGLGLGCVVCSIALF-LYFRAQMDPNRISEDSTHCFYR 68
                                                                                                   KQLTVKRQGLYYIYAQVTFCSNREASSQAP-----FTASLCLKPPNREERILLRAAN
                                                                        K-LRVNQDGFYYLYANICF-RHHETSGSVPTDYLQLMVYVVKTSIKIPSSHN--LMKGGS
                                                                                                                          MEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHKVTLSSWYHDRGWAKISN--MTLSNG
                                                                                                                                                   --NLHEDFVFM-KTIQRCNTGERSLSLLNCEEIKSQFEGFV-KDIM-----LNKEEKK 106
                                                                                                                                                                           ILRLHENADLQDSTLESEDTLPDS-----CRRMKQAFQGAVQKELQHIVGPQRFSGAPAM 123
                                                                                                                                                                                                     PVPRSAATGPP--VSMKIFMYLLTVFLITQMIGSALFAVYLHRRLD--KIEDER-----
 TH--
                       TKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKV
-SSAKPCGQQSIHLGGIFELQPGASVFVNVTDPSQVSHGTGFTSFGLLKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             285
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                                                                                                                                                                                                                                                         11.9%; Score 186.5; DB 6
26.3%; Pred. No. 3.8e-09;
Live 50; Mismatches 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                            and homology analysis of stimulatory molecules.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                       10CA588D923754EB CRC64;
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                                                                                                                                                                                                                                                                                  DB 6;
                                                                                                                                                                                                                                                           115;
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       261
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RESULY 11
O9MYL6
AC O9MYL6
AC O9MYL6
DT 01-OCT
DT 01-OCT
DT 01-DCT
DT 01-EX
OS MACACA

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                                                        C Q9MYLL;

O1-OCT-2000 (TrEMBLrel. 15, Created)

O1-OCT-2000 (TrEMBLrel. 15, Last sequence update)

O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)

P O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)

P FAS LIGAND.

PT-PASL OR CM-FASL OR RM-FASL.

Macaca nemestrina (Pig-tailed macaque),

S Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey), and

S Macaca fascicularis (Crab eating macaque)

S Macaca mulatta (Rhesus macaque).

S Macaca mulatta (Rhesus macaque).

C Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;

C Cercopithecinae; Macaca.

N NCBI_TaxID-9545, 9541, 9544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 77
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O9BDM3;
01-JUN-2001 (Tr
01-JUN-2001 (Tr
01-DEC-2001 (Tr
CD154 PROTEIN.
SEQUENCE FROM N.A.
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SMART; SM00207; TNF; 1.
PROSITE; PS00251; TNF_1; 1.
PROSITE; PS50049; TNF_2; 1.
SEQUENCE 261 AA; 29357 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fas/Fas ligand and co-stimulatory Immunogenetics 53:315-328(2001). EMBL; AF944860; AAK37542.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            211
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InterPro; IPR000478; TNF_family.
Pfam; PF00229; TNF; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=21383618; PubMed=11491535;
Villinger F., Bostik P., Mayne A.E.,
Weiss W.R., Ansari A.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aotus trivirgatus (Night monkey) (Douroucouli).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Platyrrhini; Cebidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9505;
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77; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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Last annotation updat
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                                                                                                                                                           Euteleostomi;
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RESULT 12
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Best Local :
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                                               Q9BDM5;
01-JUN-2001
01-JUN-2001
01-DEC-2001
             01-JUN-2001 (TrEMBLrel. 17, Crea 01-JUN-2001 (TrEMBLrel. 17, Last 01-DEC-2001 (TrEMBLrel. 19, Last FAS ANTIGEN CD95.

Macaca mulatta (Rhesus macaque).
Eukaryota; Metazoa; Chordata; Cr.
                                                                                               Q9BDMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00251; TNF_1; 1.
PROSITE; PS50049; TNF_2; 1.
SEQUENCE 280 AA; 31367 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR01234; TNECROSISFCT
ProDom; PD002012; TNF_abc; 1.
ProDom; PD008600; TNF_5; 1.
SMART; SM00207; TNF; 1.
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InterPro; IPR003636; TNF_abc.
InterPro; IPR003478; TNF_family.
Pfam; PF00229; TNF; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kirii Y., Inoue T., Yoshino K.;
Kirii Y., Inoue T., Yoshino K.;
"Pig-tailed monkey Fas ligand mRNA, complete cds.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ datab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPECIES-M.nemestrina; STRAIN-PIG-TAILED MONKEY; Kirii Y., Inoue T., Yoshino K.;
                                                                                                                                                      275 FGLYKL 280
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                                                                                                                                                                            FGAFKV 290
                                                                                                                                                                                            KYPQDLVMME-GKMMSYCTTGQMWAHSSYLGAVFNLTSADHLYVNVSELSLVNFEESQTF
                                                                                                                                                                                                                 KIPSSHNIMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATY
                                                                                                                                                                                                                                                                                                            ELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLT--INAASIPSGSHKVTLSSW
                                                                                                                                                                                                                                                                                                                                                                                                       PHEGPLHPAPSAPAP--APPPAASRS------MFLALLGLGLGQVVCSIALF 46
                                                                                                                                                                                                                                          EDTYGIVLLSGVKYKKGGLVINETGLYFVYSKVYFRGQSCTN---
                                                                                                                                                                                                                                                               YHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVYVVKTSI
                                                                                                                                                                                                                                                                                      QIGHPSPPPE------LEW
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                                                                                                                                                                                                                                                                                                                                                                                                                                    67;
                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 21.9
67; Conservative
    Eutheria;
                                                                                              PRELIMINARY;
  Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                              11.5%;
                                            Created)
Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                  45;
 Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 179;
Pred. No. 2
           Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F0B284D61A132EB4 CRC64;
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                                                                                           280
            Vertebrata;
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.1e-08;
Cercopithecidae;
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         Euteleostomi;
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Best Local S
Matches 67
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InterPro; IPR000478; TNF_family.
Pfam; PF00029; TNF; 1.
PRINTS; PR01217; PRICHEXTENSN.
PRINTS; PR01234; TNECHEXTENSN.
PRINTS; PR001234; TNECHEXTENSN.
PRODOM; PD002012; TNF_abc; 1.
PRODOM; PD008600; TNF_5; 1.
PRODOM; PD008600; TNF_5; 1.
SMART; SM00207; TNF; 1.
PROSITE; PS000251; TNF]; 1.
PROSITE; PS00049; TNF_2; 1.
SEQUENCE 280 AA; 31377 MW; 729
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InterPro; IPR002965; P_rich_extensn.
InterPro; IPR003263; TNF_5.
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NCBI_TaxID=9544;
                                                                                                                                                                                                               O9BDN1;
O1-JUN-2001 (TrEMBLrel. 17,
O1-JUN-2001 (TrEMBLrel. 17,
O1-DEC-2001 (TrEMBLrel. 19,
CD95L PROTEIN.
                                                                                                          Cercocebus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
                                                                    Cercopithecinae;
NCBI_TaxID=9531;
                                                                                                                                                                                                                                                                                                                                         Q9BDN1
  SEQUENCE FROM N.A. MEDLINE=21383618;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVYVVKTSI 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ELQHIYGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLT--INAASIPSGSHKVTLSSW 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QLFHLQ------KELAELRESTSQKHTA------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FGAFKV 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EDTYGIVLLSGVKYKKGGLVINETGLYFVYSKVYFRGOSCTN-----LPLSHKVYMRNS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           FGLYKL 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                                                                                  Cercocebus
       PubMed=11491535;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44;
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Pred. No. 3.1e-08;
                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -KKEQRKVAHLTGKPNSRSMP-----LEW
                                                                                                                                                                                                                                                                                                                                                 280
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Best Local S
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PRINTS; PR01217; PRICHEXTENSN.
PRINTS; PR01234; TNECROSISFCT.
PRODOM; PD002012; TNF_abc; 1.
PRODOM; PD008600; TNF_5; 1.
SMART; SM00207; TNF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Willinger F., Bostik P., Mayne A.E., King C. Weiss W.R., Ansari A.A.;
"Cloning, sequencing, and homology analysis Fas/Fas-ligand and co-stimulatory molecules. Immunogenetics 53:315-328(2001).
Immunogenetics 53:315-328(2001).
EMBL, AF344847, AAK37606.1;
HSSP; P01375; 4TSV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interpro; IPR002965; P_rich_extensn.
Interpro; IPR003263; TNF_5.
Interpro; IPR003636; TNF_abc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00251; TNF_1; 1. PROSITE; PS50049; TNF_2; 1. SEQUENCE 280 AA; 31407 MW;
                                                                                                                                                                                                              Q9BDC7
Q9BDC7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000478; TNF_family.
                                                                                                                                                                            01-JUN-2001 (TREMBLIEL 17, 01-JUN-2001 (TREMBLIEL 17, 01-DEC-2001 (TREMBLIEL 19,
 SPECIES-M. mulatta, and C.torquatus atys; Villinger F., Bostik P., Mayne A.E., King C.L. Weiss W.R., Ansari A.A.; "Cloning, sequencing and homology analysis of Fas/Fas-Ligand and co-stimulatory molecules."; Immunogenetics 0:0-0(2001).
                                                                                                                                                                 CD154 PROTEIN.
                                                                                                                  Cercocebus torquatus atys (Red'orowned mangabey) (Sooty mangabey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                      Macaca mulatta (Rhesus macaque),
                                                                                                         Cercopithecinae;
                                                                                                                                                                                                                                                                                                                                                                                                       165
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Immunogenetics
                                                                        SEQUENCE FROM N.A.
                                                                                             NCBI_TaxID=9544,
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                                                                                                                                                                                                                                                                                                                                                                              EDTYGIVLLSGVKYKKGGLVINETGLYFVYSKVYFRGQSCTN--
                                                                                                                                                                                                                                                                                                                                                                                            YHDRGWAKISNWTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVYVVKTSI
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                                                                                                                                                                                                                                                                                     FGLYKL
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ilarity 21.9%;
Conservative 4
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                                                                                               Macaca.
9531;
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                                                 Mayne A.E., King C.L.,
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Last
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Pred.
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No. 4.
                            analysis of nonhuman
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Best Local
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Best Local S
Matches 73
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SMART; SM0207; TNF, 1; 1.

PROSITE; PS00251; TNF_1; 1.

PROSITE; PS50049; TNF_2; 1.

PROSITE; PS50049; TNF_2; 1.

PROSITE; PS50049; TNF_2; 1.

PROSITE; PS50049; TNF_1; 1.

PROSITE; PS50049; TNF_2; 1.

PROSITE; PS50049; TNF_1; 1.

PROSITE; PS50049; T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q95N10 PRELIMINARY; PKI; ZULIN.
Q95N10;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

Zhu N., Young Y.;

"MOLECULAR cloning and characterization of porcine Fas ligand submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AY033634; AAK56449.1; -...
SEQUENCE 282 AA; 31752 MW; F391212406AE1E7D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
48 YFRAQMDPNRISEDSTHCFYRILRLHENADLQDSTLESEDTLPDSCRRMKQAFQGAYQKE 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               212 H--SSAKPCGQOSIHLGGVFELQPGASVFVNVTDPSQVSHGTGFTSFGLLKL 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              239 KNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKV 290
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InterPro; IPR000478; TNF_family.
Pfam; PF00229; TNF; 1.
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EMBL; AF344841; AAK37600.1;
HSSP; P29965; IALY.
                                                                   53
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                                                                                                                                                        Local Similarity 21.6
es 66; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70 LRLHENADLQDSTLESEDTLPDS-----CRRMKQAFQGAVQKELQHIVGPQRFSGAPAMM 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 PAPSAPAPAPPPAASRSMFLALLGLGLGQVVCSIALFLYFRAQMDPNRISEDSTHCFYRI 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 PSPRSAATGLPVRMKIFMYLLTIFL-ITQMIGSALFAVYLHRRLD--KIEDER-----
                                              PPPPPLLPSRPLP-PLPPPSLKKKRDHNAGLCLLVMFFMVLVALVGLGLG-----MFQ 104
                                                                             -LRVNQDGFYYLYANICF-RHHETSGSVPTDYLQLMVYVVKTSIKIPSSHN--LMKGGST 238
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                                                                                                                                                   11.1%; Score 173; DB 21.6%; Pred. No. 7.4e tive 45; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.2%; Score 174.5; DB 6;
25.0%; Pred. No. 4.8e-08;
tive 51; Mismatches 119;
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                                                                                                                                                                             DB 6;
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                                                   226 IPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYF 285
                                     219 YPODIVLME-GKMMNYCTTGQMWARSSYLGAVFNLTSADHLYVNVSELSLVNFEESKTFF
                                                                                  165 DTYGIALVSGVKYMKGSLVINDTGLYFVYSKVYFRGQYCNNQ-----PLSHKVYTRNSR 218
                                                                                                       166 HDRGWAKISNWTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVYVVKTSIK 225
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Homo sapiens
Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Primates;
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EAOPFAHLTINATDLFSGSHKVSLSSWYHDRGWAKISMMTFSNGKLIVNODGFYYLYA
NICFRHHETSGDLATEYLOLMVYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSIN
VGGFFKLRSGEEISIEVSNPSLLDPDQDATYFGAFKVRDID"
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/db_xref="taxon:9606"
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Pred. No. 5.6e-188;
Mismatches 0;
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Determination of human
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                 Unpublished
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                                                                   : 81-3-5803-0123)
                  /organism="Homo sapiens"
/db_xref="taxon:9606"
81. .1034
/gene="hRANKL
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uman RANKL isoforms
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Ikeda, T. and Kuroyama, H. Direct Submission
Submitted (25-JUN-2001) Tohru Ikeda, Tokyo Medical and Dental University, Department of Pathology and Immunology, Graduate School; Yushima 1-5-45, Bunkyo, Tokyo 113-8519, Japan (E-mail:toru.pth2@med.tmd.ac.jp, Tel:81-3-5803-5176, Craniata; Vertebrata; Catarrhini; Hominidae, Hominidae; Euteleostomi; PRI 26-DEC-2001 f nuclear factor

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 GGCCCCGGAGCCCCGAGGGCCCCCTGCACGCCCCGCCGCCGCCTGCGCCCCACCAG
                            ATGCGCCGCGCCAGCAGAGACTACACCAAGTACCTGCGTGGCTCGGAGGAGATGGGCGC
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AF019047
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Cosman, D., DuBose, R. and
Direct Submission
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Tometsko, M.E., Roux, E.R.,
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/CTANSJACTON "MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPPAPHOPPAA
RYSMFYALLIGLGGVYCSVALFFYFRAOMDPNRISEDGTHCIYRILKHENADFQDT
TLESQDTKLIPDSCRRIKOAFQGAVQKELQHIVGSQHIRAEKAMVGSWLDLAKRSKL
EAQPFAHLTINATDIPSGSHKVSISSWYHDRGWAKISNNTFSKGKLIVNQDGFYYLYA
NICERHHETSGDLATEYLQLMYVYKTSIKLESSHTLMKGGSTKYWSGNSEFHFYSIN
VGGFFKLRSGGEEISTEVLSNPSLLDPDQDATYFGAFKVRDID"

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Eutheria;
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/note="receptor activator
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pred. No. 6.1e-188;
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Lacey,D.L., Timms,E., Tan,H.-L., Kelley,M.J., Dunst;
                                   human.
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Homo saplens osteoprotegerin
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                          Euteleostomi;
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GAAGCTCAGCCTTTTGCTCATCTCACTATTAATGCCACCGACATCCCCATCTGGTTCCCAT
                                                                       CAGGCCTTTCAAGGAGCTGTGCAAAAGGAATTACAACATATCGTTGGATCACAGCACATC
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Amgen Center Drive, Thousand Oaks, California 91320, U
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/protedict="csteoprotegerin ligand"
/protedi_id="AcC39731.1"
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/db_xref="GI:3057146".1"
/db_xref="GI:3057146".1"
/db_xref="GI:3057146".1"
/translation="MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPPAPHQPPAA
/translation="MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPPAPHQPPAA
/translation="MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPPAPHQPPAA
SRSMFYALLGLGLGGOVVCSVALAFFYFRQMDPNRISEDGTHCIYRILRLHENADPQDT
TLESQDTKLIPDSCRRIKQAFQGAVQKELQHIVOSQHIRAEKAMVDGSWLDLAKRSKL
EAQPFAHLTINATDIPSGSHKYSLSSWYHDRGWAKISNMFFSNGKLIVNQDGFYYLVA
NICPRHHETSGDLATEYLQLAWYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSIN
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                                                                                                                                                                                                                                                        Direct Submission
Submitted (02-MAY-2001) Tohru Ikeda, Graduate School, Tokyo Medical and Dental University, Pathology and Immunology; 1-5-45 Yushima, Bunkyo-ku, Tokyo 113-8519, Japan (E-mail:toru.pth2@med.tmd.ac.jp, Tel:81-3-5803-5176, Fax:81-3-5803-0123)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
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Homo sapiens mRNA for hRANKL
AB061227
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Ikeda, T. and Kuroyama, H.
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                                                                         /Protein_id="BAB71768.1"
/db_xref="G1:16610213"
/db_xref="G1:16610213"
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vnodgfyklyanicfrhhetsodlatevlolmvyvtktsikipsshtlakkggtkyws
onsefhfysinvogffklarsgeelsievsnpslldpdodatyfgafkvrdid"
a 211 c 217 g 230 t
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/db_xref="taxon:9606"
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RESULT AB064270

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AB064270 Homo sapiens h factor kappa H AB064270 AB064270.1 Gi

972 bp mRNA hRANKL 2-2 mRNA for receptor B ligand 2-2, complete cds.

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TAAAGTGAGTCTGTCCTCTTGGTACCATGATCGGGGTTGGGCCAAGATCTCCCAACATGAC
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Submitted (25-JUN-2001) Tohru Ikeda, Tokyo Medical and Dental University, Department of Pathology and Immunology, Graduate School; Yushima 1-5-45, Bunkyo, Tokyo 113-8519, Japan (E-mail:toru.pth2@med.tmd.ac.jp, Tel:81-3-5803-5176, Fax:81-3-5803-0123)
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VNQDGFYYLYANICFRHHETSGDLATEYLQLMVYVTKTSIKIPSSHTLMKGGSTKYWS
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                                                                                                                                                                                                                                                                                                         Submitted (25-JUN-2001) Tohru Ikeda, Tokyo Medical and Dental University, Department of Pathology and Immunology, Graduate School; Yushima 1-5-45, Bunkyo, Tokyo 113-8519, Japan (E-mail:toru.pth2@med.tmd.ac.jp, Tel:81-3-5803-5176,
                                                                                                                                                                                                                                                                                                                                                                          Ikeda, T. and Kuroy
Direct Submission
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Homo sapiens hRANKL 3 mRNA for 1
kappa B ligand 3, complete cds.
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       /Protein_id="Bab79693.1"
/db_xref="GI:18143517"
/db_xref="GI:18143517"
/translation="mbpNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCR
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PSGSHKVSLSSWYDRRGWAKISNMTFSNGKLIVNQDGFYYLVANICFRHHETSGDLAT
EYLQLMYYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISI
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/product="receptor activator of
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sOdf/trance; sODF/TRANCE.
Homo sapiens male tongue
cell_line:SCC-4 cDNA to m
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Homo sapiens mRNA
AB037599
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Eutheria; Primates;
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Nagai,M.,
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Direct Submission
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llarity 100.0%; Pred. No. 2.3e-143;
Conservative 0; Mismatches 0;
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/cell_type="epithelial-like
/tissue_type="tongue"
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/db_xref="taxon:9606"
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Submitted (26-JAN-2000) Masazumi Nagai, Iwate Medical Unive School of Dentistry, Department of Biochemistry: 19-1 Uchim Morioka, Iwate 200-6505, Japan (E-mail:mnagaidiwate-med.ac. Tel:+81-19-651-5111(ex.4436), Fax:+81-19-654-4147)

Location/Qualifiers
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Cancer cells responsible for humoral hypercalcemia express encoding a secreted form of ODF/TRANCE that induces osteoc
                                                                                                                                   /product="sode/Trance"
/product="sode/Trance"
/protein_id="BAA90488.1"
/protein_id="BAA90488.1"
/db_xref="g1:6863048"
/translation="mdpenrisedgthCiyrilrlhenadfqDttlesQDtklipdsCr
RIKQAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDI
PSGSHKYSLSSWYHDRGWAKISNNTFSNGKLIVNQDGFYYLYANICFRHHETSGDLAT
EYLQLMYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISI
EYSNPSLLDPDQDATYFGAFKVRDID"
a 184 c 200 g 260 t 3 others
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 2390)
Ashkenazi, A. J., Goddard, A., Godowski, P. J., Gurney, A. I.
Hillan, K. J., Marsters, S. A., Pan, J., Pitti, R. M., Roy, N
Stone, D. M., Watanabe, C. K. and Wood, W. I.
Compositions and methods for the treatment of tumour
Patent: WO 0153486-A 41 26-JUL-2001;
Genentech, Inc. (US)
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/db_xref="taxon:9606"
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                                                                                                                                                                                 Wong,B.R., Rho,J., Arron,J., Lee,S.Y., Robinson,E. and (Direct Submission Submitted (09-JUL-1997) Howard Hughes Medical Institue, Rockefeller University, 1230 York Ave., New York, NY 100 Location/Qualifiers
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Homo sapiens TNF-related ligand TRANCE mRNA, partial
AF013171 GI:2411499
                                                                                                                                                                                                                                                               TRANCE is a novel ligand of the tumor necrosis factor receptor family that activates c-Jun N-terminal kinase in T cells J. Biol. Chem. 272 (40), 25190-25194 (1997) 97460112
                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1823)

Wong, B.R., Rho, J., Arron, J., Robinson, E., Orlinick, J., Chao, M., Kalachikov, S., Cayani, E., Bartlett, F.S. III, Frankel, W.N., Lee, S.Y.
                                                                                                                                                                                                                                                                                                                and Choi, Y.
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/product="Trance"
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/db_xref="GI:2411500"
/translation="QMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSC
                                                                             /note="encodes <1. .738
                                                                                                                /cell
                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="13"
                                                               /note="TNF-related ligand"
                                                    codon_start=1
                                                                                                                           /map="13q14"
                                                                                                    ert_type="thymocyte" .738
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ATCAGAGCAGAGAAAGCGATGGTGGATGGCTCATGGTTAGATCTGGCCAAGAGGAGGAACAAG
                                       AAACAAGCCTTTCAAGGGGCCGTGCAAAGGGAATTACAACACATTGTGGGGCCACAGCGC
                                                      AAACAGGCCTTTCAAGGAGCTGTGCAAAAGGAATTACAACATATCGTTGGATCACAGCAC
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Rattus norvegicus
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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Xu, J.K. and Zheng, M
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Australia, Monash Ave., Nedlands, WA
Location/Qualifiers
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/db_xrcf="taxon:10116"
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Submitted (13-AUG-1997) Molecular Biology,
                                                                                                                                                                                                                                                                                                                                                                                            Anderson, D.M.,
Tometsko, M.E.,
Gallbert, L.
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(RANKL) mRNA,
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Mammalia; Eutheria; Rodentia;
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/product="RANKL"
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/db_xref="GI:2612924"
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                                                              ligand"
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/db_xref="taxon:10090"
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ICFRHHETSGSVPTDYLQLMVYVVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINV

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TTTTTCAAGCTCCGAGCTGGTGAAGAAATTAGCATTCAGGTGTCCAACCCTTCCCTGCTG
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Eukaryota; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 951)

RS Mizuno, A., Kodaira, K. and Kodaira, Y.

DNA and process for producing protein by using the same
Patent: JP 2000102390-A 5 11-APR-2000;
SNOW BRAND MILK PROD CO LTD, YS NEW TECHNOLOGY LAB

OS Mus sp. (mouse)
PN JP 2000102390-A/5
PD 11-APR-2000
PF 30-SEP-1998 JP 1998292971
PF ATSUKO MIZUNO, KUNIHIKO KODAIRA, YASUKO KODAIRA PC
C12N15/09, A6IK31/00, C07K14/47, C12P21/02, C12Q1/68//(C12N15/09, PC
C12R1:91), A6IK31/00, C07K14/47, C12P21/02, C12Q1/68//(C12N15/09, PC
FH Key

I CCation/Qualifiers

FT SOURCE

/Organism='Mus sp. (mouse)'.
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DNA and process for producing
E34350 G:18624335
JP 2000102390-A/5.
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                                                              TTTTTAAGTTACGGTCTGGAGAGGAAICAGCATCGAGGTCTCCAACCCCTCCTTACTG 897
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ligand (RANKL) encoding			BP.	ALIGNMENTS	AAA38005 AAD18398 AAD18399 AAD03112	AAA39153 AAC67833 AAC67832	AAA39152 AAX56001	AAZ99973 AAZ99971 AAZ99970	AAZ99969 AAZ99972	AAZ99967 AAZ99968	AAV69898 AAS13369 AAA39155	AAD05903 AAH25526	AAV41371 AAD15310 AAD08714	AAX80224 AAV41377	AAV70284 AAZ99966	AAV69886 AAV41489	902	AAA39156 AAZ99965	990	AAX80223 AAF86481
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Homo sapiens.

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14-OCT-1997; 23-DEC-1996; 07-MAR-1997; 22-DEC-1997; 02-JUL-1998. WO9828426-A2. 97US-0064671. 96US-0059978. 97US-0813509. 97WO-US23775 /*tag- a
/product-Location/Qualifiers
1..954 /*tag-"human RANKL (ligand for RANK)"

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This cDNA encodes a human RANKL, a ligand for the RANK (receptor CC activator of necrosis factor-kappaB (NF-MB)) polypeptide. RANK is a CC member of the tumour necrosis factor (TNF) family. A soluble RANK CC member of the tumour necrosis factor (TNF) family. A soluble RANK CC may be used for inhibiting activation of NF-MB, by contacting a cell CC expressing membrane-associated RANK with a soluble RANK which binds to CC RANK ligand (RANKL). RANKL polypeptides can activate RANK and can be CC used to induce maturation of dendritic cells and enhance their CC soluble RANK polypeptide composition may also be used for regulating an collaboration of inflammatory response. Inhibition of NF-MB by RANK antagonists CC immune or inflammatory response. Inhibition of NF-MB by RANK antagonists CC response that result from triggering of RANK, e.g. in treating toxic reactions. They can also be used in adjunct therapy for disease CC characterised by neoplastic cells that express RANK. RANKL polypeptides can also be used to identify inhibitors of RANK and thus inhibitors of CC an inflammatory response, and also for protecting RANK-expressing cells from the negative effects of chemotherapy or the presence of high levels of TMF-alpha. The products can also be used for detection and drug
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07-MAR-1997;
14-OCT-1997;
23-DEC-1996;
07-MAR-1997;
22-DEC-1997;
                                                                               New receptor activator of NF-kappaB (RANK) polypeptides, useful regulating immune response, in screening for RANK inhibitors, or adjunct therapy for disease characterized by neoplastic cells the express RANK.
                                                                                                                                                                                     AWWI)
                                                                                                                                                                                                                                                                                                                                                                                                                Human; receptor activator of nuclear factor kappaB ligand; RANKL; NF; tumour necrosis factor; TNF; receptor associated factor; TRAF; immune response; inflammatory response; graft-versus-host reaction; toxic shock; sepsis; acute inflammatory reaction; bone resorption; anti-apoptotic signal; therapy; immunosuppressant; anti-inflammatory;
                                                                                                                                                                                                                                                                                                      07-AUG-2001.
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97US-0077181.
97US-0064671.
97US-0772330.
96US-0772330.
97US-0813509.
97US-0996139.
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/*tag= a
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The patent discloses novel receptor activator of nuclear factor (NF)-kappaB (RANK) proteins and their corresponding DNAs. RANK is a member of the tumour necrosis factor (TNF) receptor superfamily and associates with TNF receptor associated factor (TRAF) 2 and 3 which are important in the regulation of immune and inflammatory response. The receptors

Example

7;

Column

69-71;

47pp;

English.

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cc molecules that inhibit interaction of RANK with TRAFI, TRAF3, CC TRAF5 and particularly TRAF5. NF kappaB inhibition by RANK antagonists care useful in ameliorating the negative effects of an inflammatory consists of special result from triggering of RANK, e.g. in treating toxic consoled or sepsis, graft-versus-host reactions, acute inflammatory creactions and the effects of bone resorption. RANK acts as an anti-cc apoptotic signal and rescue the cells that express RANK from apoptosis. Cc soluble forms of the receptor are used in vivo or in vitro based cc screening tests for agonists or antagonists of RANK activity, as antagonists of RANK-mediated NF-kappa B activation, or to inhibit capping the form of a signal via RANK. Compositions are used in the development of both agonistic and antagonistic antibodies, or as an cappuress RANK. Compounds that interfere with RANK-TRAF6 interactions care useful for modulating the formation of osteoclasts from osteoclast precursors and for modulating osteoclast function and activities. They care used as inhibitors of disease associated with excess bone resorption and as immunosuppressants or anti-inflammatory agents. The RANK DNAs are useful for the expression of recombinant proteins, as probes for analysis of the presence or distribution of RANK transcripts, while the proteins care useful in preparing kits for the detection of soluble RANK, or monitor RANK-related activity. The present sequence is a cDNA encoding complete the protein activity agents.
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AAAGTGAGTCTGTCCTCTTGGTACCATGATCGGGGTTGGGCCAAGATCTCCAACATGACT
                                                      gaagctcagccttttgctcatctcactattaatgccaccgacatcccatctggttcccat
                                                                         GAAGCTCAGCCTTTTGCTCATCTCACTATTAATGCCACCGACATCCCATCTGGTTCCCAT
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                                                                                                                                            AGAGCAGAGAAAAGCGATGGTGGATGGCTCATGGTTAGATCTGGCCAAGAGGAGCAAGCTT
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Pred. No. 5e-241;
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The present invention relates to receptor activator of NF-chi B DNA. RANK is mapped to chromosome 18q22.1 and its ligand (RANKL) chromosome 13q14. RANK and RANKL are type 1 and type 2 transmemb

B (RANK)

Claim

2

Column

61-64;

43pp; English

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07-MAR-1997;
14-OCT-1997;
                                                                                                                                                                                                                                                                                        Human; receptor activator of NF-chi B; RANK; tumour necrosis factor; CD40; TNF receptor-associated factor; TRAF; ligand; immune response; chromosome 18q22.1; huRANKL; chromosome 13q14; transmembrane protein
                                                                                                                           AWWI)
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                                                                                                                                                                                                                                                                                                                                            04-SEP-2001
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                                               molecules, useful for producing ligands (which are ing immune response and in screening for inhibitors ractivator) of the receptor activator of NF-chi B
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97US-0077181.
97US-0064671.
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TTTAAGTTACGGTCTGGAGAGGAAATCAGCATCGAGGTCTCCAACCCCTCCTTACTGGAT
                                    accaagtattggtcagggaattctgaattccatttttattccataaacgttggtggattt
                                                ACCAAGTATTGGTCAGGGAATTCTGAATTCCATTTTATTCCATAAACGTTGGTGGATTT
                                                                                     tacgtcactaaaaccagcatcaaaatcccaagttctcataccctgatgaaaggaggaagc
                                                                                                   TACGTCACTAAAACCAGCATCAAAATCCCAAGTTCTCATACCCTGATGAAAGGAAGC
                                                                                                                                       tgctttcgacatcatgaaacttcaggagacctagctacagagtatcttcaactaatggtg
                                                                                                                                                    TGCTTTCGACATCATGAAACTTCAGGAGACCTAGCTACAGAGTATCTTCAACTAATGGTG
                                                                                                                                                                                                      TTTAGCAATGGAAAACTAATAGTTAATCAGGATGGCTTTTATTACCTGTATGCCAACATT
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of NF-kappaB ligand) protein"
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New DNA encoding a receptor activator of NF-kappaB polypeptide treatment of Paget's disease and Familial Expansile Osteolygis New DNA WPI; 2001-329222/34 Anderson DM, 17-NOV-1999; 14-NOV-2000; (IMMV) IMMUNEX AAE01993 2000WO-US31459 Hughes 99US-0442029 CORP ΑE Expansile

Example

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96pp;

English.

Osteolysis

for the 'FEO' (FEO)

CC (receptor activator of NF (nuclear factor) -kappaB), a member of TNF CC (tunour necrosis factor) receptor superfamily. RANK is a Type I CC transmembrane protein that interacts with TNF receptor-associated CC factors (TRAFS). Triggering of RANK by overexpression or co-expression of RANK and membrane bound RANK ligand (RANKL) results in upregulation CC of the transcription factor NF-kappaB, a ubiquitous transcription factor CC that is most extensively utilised in cells of the immune system. CC inhibition of Nf-kappaB by RANK antagonists is useful in ameliorating CC negative effects of inflammatory reactions, and the effects of excess cone resorption. The RANK DNAs, proteins and their analogues are useful CC cells for use in gene therapy applications in diagnosing diseases associated with RANK, and as targets for use in screening assays. They can be used in the treatment or diagnosis of immune system dysfunction. The present invention also encompasses gene therapy methods to correct costeolysis (PEO) and early onset paget's disease of bone (EP). The present sequence is a CDNA encoding full-length human RANKL (hurankil) cc protein. The RANKL gene is located in chromosome 13q14. The present invention relates to a novel receptor, referred RANK

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GGCCCGGAGGCCCGCACGAGGGCCCCCTGCACGCCCCGCGCCGCCGCCGCCGCACCAG

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                                                   Osteoprotegerin is a secreted member of the tumour necrosis factor receptor family, which blocks osteoclastogenesis in a dose dependent manner. The OPGL protein is synthesised as a type II transmembrane protein. The murine and human OPGL polypeptides are 87% homologous. OPGL is a potent osteoclast differentiation factor when combined with CSF-1. It is not capable of inducing osteoclast differentiation in the absence of CSF-1. OPGL is also an activator of mature osteoclasts. The specification describes a method for the in vivo down-regulation of OPGL activity in an animal. The method comprises using at least one OPGL polypeptide or subsequence, and/or at least one OPGL analogue to induce an immune response in the animal. The method and OPGL polypeptide are useful for treating, preventing and ameliorating osteoporosis or other diseases or conditions characterised by excessive bone resorption.
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02-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                          present sequence encodes a human osteoprotegerin ligand (OPGL). eoprotegerin is a secreted member of the tumour necrosis factor
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)B; AAY84417.
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                                              TACGTCACTAAAACCAGCATCAAAATCCCAAGTTCTCATACCCTGATGAAAGGAGGAAGC
ccggatcaggatgcaacatactttggggcttttaaagttcgagatatagattga
                                                                                                   accaagtattggtcagggaattctgaattccattttattccataaacgttggtggattt
                                                                                                               ACCAAGTATTGGTCAGGGAATTCTGAATTCCATTTTATTCCATAAACGTTGGTGGATTT
                                                                                                                                                    tacgtcactaaaaccagcatcaaaatccccaagttctcataccctgatgaaaggaggaagc
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11-FEB-1999
                                 AAV70285
                                standard; DNA;
                      (first entry)
                                 2274
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Human osteoprotegerin binding protein from the pcDNA/huOPGbpl.linsert.

Human; osteoprotegerin binding protein; OPG binding protein; arthritis; osteoporosis; osteoclast maturation; bone disease; metastasis; ODAR; hypercalcaemia; osteoclast differentiation and activation receptor; Paget's disease; 88.

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CC Host cells transfected with vectors containing nucleic acid molecules
CC encoding OPG binding protein are used to produce recombinant OPG binding
CC protein. OPG binding protein is used in binding assays to determine
CC osteoprotegrin (OG) in biological samples; to screen for specific
CC binding agents (particularly agonists and antagonists, including
CC intracellular proteins); to raise Ab (useful in immunoassays for
CC detection of OPG binding protein) and to identify compounds that
CC modulate binding of OPG binding protein to osteoclast differentiation
CC and activation receptor (ODAR). The nucleic acid molecule encoding OPG
CC binding protein can be used to detect OPG binding protein-encoding
CC sequences, e.g. screening for related sequences, also to produce
CC transgenic animal models, while complementary sequences are used for
CC antisense regulation of OPG binding protein expression. Modulators of
CC OPG binding protein, particularly soluble forms of OPG binding protein
CC or Ab, are used to treat or prevent bone diseases, e.g. osteoporosis,
CC bone loss caused by arthritis or metastases, hypercalcaemia, Paget's
CC disease, periodontal disease, osteoporosis, lossening of prostheses,
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16-APR-1997;
23-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                   e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid encoding osteoprotegrin binding protein - useful for, e.g. treating bone diseases by modulating osteoclast differentiation
                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Fig 4; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB;
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                                                                                                                                                                                                                                                                                                                                        present sequence encodes human osteoprotegerin (OPG) binding protein
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DB; AAW83195.
                                                                                                                                                                                                                                                                                                                                                                                                                 diagnosis
                               in
                           combination with agents that promote bone
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97US-0842842.
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Sequence 2274 B₽; 658 A; 463 Ç 523 G; 630 Ŧ, 0 other;

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GAAGATGGCACTCACTGCATTTATAGAATTTTGAGACTCCATGAAAATGCAGATTTTCAA
                                                                CCCCCGCCGCCTCCATGTTCGTGGCCCTCCTGGGGCTGGGGCTGGGCCAGGTT
                                                                                                                                                                          ATGCGCCGCCCAGCAGAGACTACACCAAGTACCTGCGTGGCTCGGAGGAGATGGGCGGC
                                  GTCTGCAGCGTCGCCCTGTTCTTCTATTTCAGAGCGCAGATGGATCCTAATAGAATATCA
                                                                                                               ggccccggagccccgcacgagggccccctgcacgcccccgccgcctgcgccgcaccag
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                      gtotgcagcgtcgccctgttcttctatttcagagcgcagatggatcctaatagaatatca
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ilarity 100.0%;
Conservative
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                                                                                                                                                                                                            Score 954; DB 19;
Pred. No. 7.1e-241;
Mismatches 0;
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                                                                                                                                                                                                                                                                               osteoclast;
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09-JUN-1997;
12-AUG-1997;
21-AUG-1997;
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   Goto M,
Nakagawa
Washida N
                                                                                                            02-DEC-1997;
15-APR-1997;
09-JUN-1997;
12-AUG-1997;
21-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Osteoclastogenesis
                                                                          (SNOW)
                                                                                                                                                                                                                       15-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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                   Higashlo K,
N, Shima N,
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/*tag= a
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Takahashi K,
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Kobayashi F,
K, Tomoyasu A,
Yasuda H;
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The present sequence encodes an osteoclastogenesis inhibitory factor (OCIF)-binding molecule (OBM). The protein promotes and supports the Separation and maturation of osteoclasts in the presence of bone 2C absorption factors such as calcitriol or parathyroid hormone (PTH). COBM is isolated from stroma cells cultured in the presence of a bone 2C absorption factor by separation and solubilisation of membrane proteins 2C then affinity chromatography using OCIF. It exists in a full-sequence 2C form and a solubilised form (sOBM) which is a shorter chain. OBM may be 2C used for screening potential inhibitors and modifiers of its biological 2C These substances can then be used in the treatment of disorders of bone 2C used for calcium metabolism. The antibodies can be used for assay 2C of the protein, for investigative and diagnostic purposes, and as 2v vv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 199
P-PSDB;
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DB; AAW83020.
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m metabolism
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Sequence 741 ₽₽; 230 Α; 153 Ç 158 9 200 1. 0 other;

Query Match Best Local

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                                                              GCTACAGAGTATCTTCAACTAATGGTGTACGTCACTAAAACCAGGATCAAAATCCCAAGT
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TTTTATTCCATAAACGTTGGTGGATTTTTTAAGTTACGGTCTGGAGAGGAAATCAGCATC
                  tctcataccctgatgaaaggaagcaccaagtattggtcagggaattctgaattccat
                                TCTCATACCCTGATGAAAGGAAGGAAGCACCAAGTATTGGTCAGGGAATTCTGAATTCCAT
                                                                                                            ggcttttattacctgtatgccaacatttgctttcgacatcatgaaacttcaggagaccta
                                                                                                                       GGCTTTTATTACCTGTATGCCAACATTTGCTTTCGACATGATGAAACTTCAGGAGACCTA
                                                                                                                                                        ggttgggccaagatctccaacatgacttttagcaatggaaaactaatagttaatcaggat
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RESULT 1
 11-DEC-1998;
12-DEC-1997;
03-MAR-1998;
                                The present sequence encodes human TNF-related activation induced cytokines (TRANCE). Human or murine TRANCE polypeptides or their variants, fragments, derivatives or analogues may be used as modulators of immune response in a mammal comprising, antisense sequences to TRANCE and fusion proteins comprising human and/or murine TRANCE. Agonists and antagonists of TRANCE, can be used to modulate immune response by increasing or decreasing the life span of mature dendritic cells and increasing or decreasing T cell activation. These techniques are especially useful for treating immune system related conditions such as HIV, cancer, autoimmune disease or hypersensitivity to an allergen. The TRANCE polypeptides can be used to increase the viability of dendritic cells in vivo or in vitro, especially when used in conjunction with proteins of the tumour necrosis factor (TNF) superfamily (especially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Key
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Sequence 1823
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                                                   aaacaagcctttcaaggggccgtgcaaagggaattacaacacattgtggggccacagcgc
                                                                                                                  CAAGACACTCTGGAGAGTCAAGATACAAAATTAATACCTGATTCATGTAGGAGAATT
                                                                                                                                                                                                     ATCAGAGCAGAGAAAGCGATGGTGGATGGCTCATGGTTAGATCTGGCCAAGAGGAGGAGCAAG
                                                                 AAACAGGCCTTTCAAGGAGCTGTGCAAAAGGAATTACAACATATCGTTGGATCACAGCAC
                                                                                                                                                                  TCAGAAGATGGCACTCACTGCATTTATAGAATTTTGAGACTCCATGAAAATGCAGATTTT
                                                                                                   caggactcgactctggagagcgaagacacagaagcactacctgactcatgcaggagaatg
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                                                                                                                                                                                                                                                                     CAGCCCCCCCCCCCCCCCCCCTCCATCTTCCTGGCCCTCCTGGGGCTGGGCCTGGGCCAG
                                                                                                                                                                                                                                                                                                          tgccctggcgtcccacacgagggtccgctgcatcccgcgccttcagcaccggctccagcg
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DB; AAB82092.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid encoding rat osteoclast differentiation factor for modulating activity of a cell, e.g., cell proliferation, differentiation and cell viability
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0; Mismatches
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hes 166;
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15-APR-1997;
09-JUN-1997;
12-AUG-1997;
21-AUG-1997;
                    Protein binding to osteoclastogenesis for, e.g. treatment and investigation calcium metabolism
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a N, Shima N,
N, Yamaguchi
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97JP-0097808.
97JP-0151434.
97JP-0217897.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        an osteoclastogenesis inhibitory factor (OCIF)-binding molecule (OBM). The protein promotes and supports the separation and maturation of osteoclasts in the presence of bone absorption factors such as
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                                               The present invention describes a genomic DNA encoding a protein having an activity of supporting or promoting differentiation and maturation of consteoclasts. The genomic DNA encoding a protein has the following properties: (a) combines specifically with osteoclastogenesis inhibitory factor (OCIF) and has a high affinity; (b) shows a molecular weight (mw) of 30,000 to 40,000 by SDS-PAGE (sodium dodecyl sulfate-polyacrylamide yel electrophoresis) under a nonreductive condition and the apparent mw when crosslinked with monomer type OCIF is 90,000 to 110,000; and (c) has an activity of supporting or promoting differentiation and maturation of osteoclast in the co-culture of mouse osteoblast-like stroma cell and consuse spleen cell in the presence of a bone absorption promoting factor such as active type vitamin D3 and parathyroid hormone (PTH). The protein can be used as a drug and a research reagent. The present sequence encodes a mouse OCIF binding molecule (OBM) from the present invention.
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Osteoprotegerin is a secreted member of the tumour necrosis factor, receptor family, which blocks osteoclastogenesis in a dose dependent manner. The OPGL protein is synthesised as a type II transmembrane protein. The murine and human OPGL polypeptides are 87% homologous. OPGL is a potent osteoclast differentiation factor when combined with CSF-1. It is not capable of inducing osteoclast differentiation in the absence of CSF-1. OPGL is also an activator of mature osteoclast. The specification describes a method for the in vivo down-regulation of OPGL activity in an animal. The method comprises using at least one OPGL polypeptide or subsequence, and/or at least one OPGL analogue to induce an immune response in the animal. The method and OPGL polypeptide are useful for treating, preventing and ameliorating osteoporosis or other diseases or conditions characterised by excessive bone resorption.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Osteoprotegerin ligand; OPGL; osteoprotegerin; osteoclastogenesis; tumour necrosis factor receptor; type II transmembrane protein; osteoclast differentiation; CSF-1; osteoclast activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Key
                                                                                                                                                                                                                                                                                                                                                                                                                                            15-SEP-1998;
02-OCT-1998;
 Sequence
                                                                                                                                                                                                                              The present sequence encodes a murine osteoprotegerin ligand (OPGL).
                                                                                                                                                                                                                                                            Disclosure;
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              GTTGTCTGCAGCGTCGCCCTGTTCTTCTATTTCAGAGCGCAGATGGATCCTAATAGAATA
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gtggtctgcagcatcgctctgttcctgtactttcgagcgcagatggatcctaacagaata
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 951
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                                               atttgctttcggcatcatgaaacatcgggaagcgtacctacagactatcttcagctgatg
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1: /cgn2_6/ptodata/2,
2: /cgn2_6/ptodata/2,
3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
5: /cgn2_6/ptodata/2,
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954
                             GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen
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/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/BCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/backfiles1.seq:*
   DB
  US-08-996-139-12
US-08-995-659-12
US-09-215-649A-12
US-09-052-521C-1
US-08-984-284-6
US-09-052-521C-1
US-08-995-659-10
US-09-995-659-10
US-09-320-424-10
US-08-584-031-2
US-08-780-496-2
US-08-670-354-1
US-09-320-424-1
PCT-US96-10895-1
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Sequence 6, Appl
Sequence 10, Appl
Sequence 10, Appl
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Sequence 12, Appl
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US-08-479-041-23	US-08-479-383-23	US-08-470-354-23	US-08-479-382-23	US-08-474-556-23	US-08-471-601-23	US-08-952-061-1	US-08-652-426A-1	US-09-040-738-1	US-08-717-294-42	US-08-474-933-1	US-08-125-468-1	PCT-US95-05008-1	US-08-426-509A-1	US-08-804-198-1	US-08-804-227C-7	US-08-951-742-5	US-08-265-310-5
Sequence 23, Appl		Sequence 1, Appli	<u>-</u> -	Sequence 1, Appli	Sequence 42, Appl	Sequence 1, Appl1	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	۲,	7,	'n	Sequence 5, Appl1				

ALIGNMENTS

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CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 60/064,671

FILING DATE: 14 OCTOBER 1997

PRIOR APPLICATION NUMBER: USSN 08/813,509

FILING DATE: 07 MARCH 1997

PRIOR APPLICATION NUMBER: USSN 08/772,330

FILING DATE: 23 DECEMBER 1996

ATTORNEY/AGENT INFORMATION:

NAME: PERKINS, PATTICIA Anne

REGISTRATION NUMBER: 2851-A

TELEPHONE: (206)33-0644

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 908 bases

LENGTH: 908 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating
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APPLICATION NUMBERS OF THE PROPERTY APPLICATION DATA:
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APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
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LENGTH: 954 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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22 DECEMBER 1997
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Best Local Similarity
Matches 954; Conserv
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                     ACCAAGTATTGGTCAGGGAATTCTGAATTCCATTTTATTCCATAAACGTTGGTGGATTT
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  TTTAAGTTACGGTCTGGAGAGGAAATCAGCATCGAGGTCTCCAACCCCTCCTTACTGGAT
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Pred. No. 2.5e-251;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                           TELEPHONE: (266)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 12
SEQUENCE CHARACTERISTICS:
                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: CDN
                                                                                                                                                                                                                                                                                                       NAME: PERKINS, PATRICIA ANN
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.
SOFTWARE: Microsoft Word for Power Macintosh
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Anderson, Dirk M. APPLICANT: Galibert, Laurent APPLICANT: Maraskovsky, Euge
                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
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APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
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                                                                                   ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
                                                                                                                                    MOLECULE N
HYPOTHETICAL: N
                                                                                                                        ORIGINAL SOURCE:
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                                              FEATURE:
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                                                           LIBRARY:
CLONE: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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                                                                                                                                                                                                                TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
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                LOCATION:
                             NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
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22 DECEMBER 1997
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RESULT 3
US-09-215-649A-12
; Sequence 12, Application US/09215649A
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Best Local Similarity
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                                                                                                                                                                                            Matches
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Best Local Similarity
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TELEPAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
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APPLICANT: Anderson, Dirk M.
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                          ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
LIBRARY: <Unknown>
CLONE: huRANKL (full length)
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COMPUTER: Apple Power MacIntosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power MacIntosh 6.0.1
CURRENT APPLICATION DATA:
      CCCCCGCCGCCTCCCGCTCCATGTTCGTGGCCCTCCTGGGGCTGGGGCTGGGCCAGGTT 180
                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
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TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
                                                                                  GGCCCCGGAGCCCCCACGAGGGCCCCCTGCACGCCCCGCCGCCGCCGCCTGCGCCCGCACCAG
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APPLICATION NUMBER: 08/996,139

FILING DATE: <UNKNOWN>

APPLICATION NUMBER: USSN 08/813,509

FILING DATE: 07 MARCH 1997

APPLICATION NUMBER: USSN 08/772,330

FILING DATE: 23 DECEMBER 1996
                                                                                                                                                                                                                                                                                                  NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/215,649A FILING DATE: 17-Dec-1998 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Immunex Corporation, STREET: 51 University Street
                                                                                                                                                                                           Conservative
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                               CURRENT APPLICATION NUMBER: US/09/052,52
CURRENT FILING DATE: 198-03-30
PRIOR APPLICATION NUMBER: 08/880,855
PRIOR FILING DATE: 1997-06-23
PRIOR APPLICATION NUMBER: 08/842,842
PRIOR FILING DATE: 1997-04-16
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                           SD
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                                                                                                                                Sequence 3, Application Patent No. 6316408 GENERAL INFORMATION:
                         SEQ ID
                                                                                                      APPLICANT: Boyle, WITTILE OF INVENTION: FILE REFERENCE: A-4
                                                                                                                                                            -09-052-521C-3
TYPE: DNA ORGANISM: Human
                 LENGTH:
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; LOCATION: (18
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ccggatcaggatgcaacatactttggggcttttaaagttcgagatatagattga
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Pred. No. 3.6e-251;
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US-08-989-362-1
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US-08-989-362-1
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Best Local Similarity
Matches 790; Conserv
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APPLICANT: Gorman, Da
APPLICANT: Mattson, J
TITLE OF INVENTION: M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 60/032,846
FILING DATE: 13-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin p.
RECISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0686
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (650)496-1204
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/989,362
FILING DATE: 12-DEC-1997
CLASSIFICATION: 56
PRIOR APPLICATION DATA:
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CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
ADDRESSE: DNAX Research Institute
STREET: 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
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CITY: Palo Alto
STATE: Californi
                      238
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STRANDEDNESS: single
TOPOLOGY: linear
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Pred. No. 1.5e-172;
0; Mismatches 158;
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GENERAL INFORMATION:
                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                             TITLE OF INVENTION: OS NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                 APPLICANT: Boyle, William
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                                              APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                             COUNTRY: USA
ZIP: 91230-1789
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STATE: California
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INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 2295 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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Best Local Similarity
Matches 790; Conserv
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Pred. No. 1.5e-172;
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; LOCATION: (158)..(1105)
US-09-052-521C-1
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US-09-052-521C-1
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TITLE OF INVENTION: Osteoprotegerin Binding Profile Reference: A-451Brv
FILE REFERENCE: A-451Brv
CURRENT APPLICATION NUMBER: US/09/052,521C
CURRENT FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 08/880,855
PRIOR FILING DATE: 1997-06-23
PRIOR APPLICATION UMBER: 08/842,842
PRIOR APPLICATION UMBER: 08/842,842
PRIOR APPLICATION UMBER: 08/842,842
PRIOR FILING DATE: 1997-04-16
NUMBER: OF SEQ. ID NOS: 40
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SEQ ID NO 1
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Best Local Similarity
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CTTGAAGCTCAGCCTTTTGCTCATCTCACTATTAATGCCACCGACATCCCATCTGGTTCC
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82.5%;
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Pred. No. 1.5e-172;
0; Mismatches 158;
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                                                                                                                                                                                   STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTMARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,139
ETITUR DATE: 22 DECEMBER 1007.
                                                                                                                                                                                                                                                                                                                                                                                                      Patent No. 6017729
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 10, Application US/08996139 Patent No. 6017729
         APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,633
REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator
NUMBER OF SEQUENCES: 19
                                                                                                                     APPLICATION NUMBER: USSN 60/064,671 FILING DATE: 14 OCTOBER 1997 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
PRIOR APPLICATION DATA:
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CLASSIFICATION:
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University Street
(206)587-0430
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22 DECEMBER 1997
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLONE: RANKL FEATURE:
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LOCATION:
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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GCTTTCGACATCATGAAACTTCAGGAGACCTAGCTACAGGAGTATCTTCAACTAATGGTGT
                                                                                                                                                 TTAGCAATGGAAAACTAATAGTTAATCAGGATGGCTTTTATTACCTGTATGCCAACATTT
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                                                                 GCTTTCGGCATCATGAAACATCGGGAAGCGTACCTACAGACTATCTTCAGCTGATGGTGT
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82.2%;
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Pred. No. 1.3e-158;
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474

654 721 594 661 534 601 481

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294 361 240 301 180 241

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Gaps

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NAME/KEY: LOCATION:

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                                                                                                                                                                                                                TELEFAX: (206)233-0644 INFORMATION FOR SEQ ID NO:
                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.
SOFTWARE: Microsoft Word for Power Macintosh
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: USSN 60/064,671
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                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION UNMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852
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                               IMMEDIATE SOURCE:
                                                                                           HYPOTHETICAL:
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                                                                 ORIGINAL
                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 1630 base pair
                                                                                  ANTI-SENSE:
                                                                                                               MOLECULE TYPE:
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CLONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US FILING DATE: 07 MARCH
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                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                 ORGANISM:
                 LIBRARY:
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                                                               SOURCE:
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51 University Street
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                                                 Mus musculus
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22 DECEMBER 1997
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              CGGATCAGGATGCAACATACTTTGGGGCTTTTAAAGTTCGAGATATAGATTGA 954
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 CGGATCAAGATGCGACGTACTTTGGGGGCTTTCAAAGTTCAGGACATAGACTGA
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Pred. No. 1
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RESULT 10 US-09-215-649A-10

Sequence 10, Application US/09215649A

294 361

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NAME/KEY: CDS
LOCATION: 3..884
SEQUENCE DESCRIPTION: SEQ
US-09-215-649A-10
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GENERAL INFORMATION:
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TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 10:
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FILING DATE: 17-Dec-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/996,139
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: <Unknown>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
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                                                                                                                                                                                                                                      Match
Local Similarity
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COMPUTER: Apple Power MacIntosh
OPERATING SYSTEM: Apple Operating System 7.5.
SOFTWARE: Microsoft Word for Power Macintosh
CURRENT APPLICATION DATA:
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LENGTH: 1630 base pa
                              TCTGCAGCGTCGCCCTGTTCTTCTATTTCAGAGCGCAGATGGATCCTAATAGAATATCAG
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                                                                                                                                                                     FEATURE:
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                                                                          CACCCCCCCCCCCCCCCATGTTCCTGGCCCCTCCTGGGGCTGGGACTGGGCCAGGTGG
            TCTGCAGCATCGCTCTGTTCCTGTACTTTCGAGCGCAGATGGATCCTAACAGAATATCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
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STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                LIBRARY: <Unknown>
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Pred. No. 1.3e-158;
0; Mismatches 150;
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APPLICANT: WILEY, Steven R.
APPLICANT: GOOGWIN, Raymond G.
TITLE OF INVENTION: CyCokine that Induces Application of the property of the company of the cycokine that Induces Application number: US/09/320,424
CURRENT FILING DATE: 1999-05-26
EARLIER APPLICATION NUMBER: 09/10,046
EARLIER FILING DATE: 1998-11-10
EARLIER FILING DATE: 1998-03-26
EARLIER FILING DATE: 1998-03-26
EARLIER APPLICATION NUMBER: 08/670,354
EARLIER APPLICATION NUMBER: 08/58,368
EARLIER APPLICATION NUMBER: 08/548,368
EARLIER APPLICATION NUMBER: 08/548,368
EARLIER APPLICATION NUMBER: 08/496,632
EARLIER APPLICATION NUMBER: 08/496,632
EARLIER FILING DATE: 1995-06-29
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver: 2.0
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SEQ ID NO 10 LENGTH: 759

TYPE: DNA
ORGANISM: synthetic fusion

FEATURE:

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51.9%;

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; NAME/KEY: CDS
; LOCATION: (1)..(759)
US-09-320-424-10
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US-09-320-424-12
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                                                         ; NAME/KEY: CDS
; LOCATION: (1)..(768)
US-09-320-424-12
                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/320,424
CURRENT FILING DATE: 1999-05-26
EARLIER APPLICATION NUMBER: 09/190,046
EARLIER FILING DATE: 1998-11-10
EARLIER APPLICATION NUMBER: 09/048,641
EARLIER FILING DATE: 1998-03-26
EARLIER APPLICATION NUMBER: 08/670,354
EARLIER APPLICATION NUMBER: 08/670,354
EARLIER FILING DATE: 1996-06-25
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Best Local S
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APPLICANT: Wiley, Steven R.

APPLICANT: Goodwin, Raymond G.

TITLE OF INVENTION: Cytokine that Induces Apoptosis

FILE REFERENCE: 2835-E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 12, Appli
Patent No. 6284236
                                                                                                                                                                      SEQ ID NO 12
LENGTH: 768
Query Match
                                                                                                                                                                                                             EARLIER APPLICATION NUMBER: 08/548,368
EARLIER FILING DATE: 1995-11-01
EARLIER APPLICATION NUMBER: 08/496,632
EARLIER FILING DATE: 1995-06-29
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                   TYPE: DNA
ORGANISM: synthetic fusion
                                                                                                                  FEATURE:
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    Score 69.4;
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; ORGANISM: Homo
US-08-584-031-2
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                 Matches 182;
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
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TITLE OF INVENTION: APO-2 LIGAND
TILE REFERENCE: 11669.22US03
CURRENT APPLICATION NUMBER: US/08/584,031A
CURRENT FILING DATE: 1996-01-09
NUMBER OF SEQ ID NOS: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1042
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CTTACTGGATCCGGATCAGGATGCAACATACTTTGGGGCTTTTAAAGTTCG
                                                agggggaatatttgagcttaaggaaaatgacagaatttttgtttctgtaacaaatgagca 881
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                                                                                  TGGTGGATTTTTAAGTTACGGTCTGGAGAGGAAATCAGCATCGAGGTCTCCAACCCCTC
                                                                                                                   aagtgctagaaatagttgttggtctaaagatgcagaatatggactctattccatctatca
                                                                                                                                         AGGAGGAAGCACCAAGTATTGGTCAGGGAATTCTGAATTCCATTTTATTCCATAAACGT 830
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Pred. No. 1.2e-09;
0; Mismatches 166;
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TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1042 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 7.3%;
Best Local Similarity 51.9%;
Matches 182; Conservative
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Patent No. 6046048
GENERAL INFORMATION:
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MEDIUM TYPE: 3.5 inch, 1.44 mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Marschang Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: PO
TELECOMMUNICATION INFORMATION:
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                                        891 CTTACTGGATCCGGATCAGGATGCAACATACTTTGGGGCTTTTAAAGTTCG 941
                                                                                                             831 TGGTGGATTTTTTAAGTTACGGTCTGGAGAGGAAATCAGCATCGAGGTCTCCCAACCCCTC
                                                                                                                                                                                                                                                                                                 711 ACTAATGGTGTACGTCACTAAAACCAGCATCAAAATCCCAAGTTCTCATACCCTGATGAA 770
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/780,496 FILING DATE: 08-Jan-1997 CLASSIFICATION: 435
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CITY: South San Francisco
STATE: California
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CTTGATAGACATGGACCATGAAGCCAGTTTTTTCGGGGCCCTTTTTAGTTGG 932
                                                                                     AGGGGGAATATTTGAGCTTAAGGAAAATGACAGAATTTTTTGTTTCTGTAACAAATGAGCA 881
                                                                                                                                                                     AAGTGCTAGAAATAGTTGTTGGTCTAAAGATGCAGAATATGGACTCTATTCCATCTATCA 821
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VENTION: Apo-2 Ligand
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Pred. No. 1.2e-09;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/496,632
FILING DATE: 29-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION UNMBER: US 08/548,368
FILING DATE: 01-NOV-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: APGETCA KETTURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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HYPOTHETICAL: N
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                          FEATURE:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Microsoft Word, Version 6.0.1 CURRENT APPLICATION DATA:
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       541
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                                                                                                                                424 CAACTTGCACTTGAGGAATGGTGAACTGGTCATCCATGAAAAAGGGTTTTACTACATCTA 483
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NUMBER OF SEQUENCES:
                                                                                                                                                      591 CAACATGACTTTTAGCAATGGAAAACTAATAGTTAATCAGGATGGCTTTTATTACCTGTA 650
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ZIP: 98101
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                               ACTAATGGTGTACGTCACTAAAACCAGCATCAAAATCCCAAGTTCTCATACCCTGATGAA 770
ACAAATGGTCCAATATATTTACAAATACACAAGTTATCCTGACCCTATATTGTTGATGAA
                                                                TTCCCAAACATACTTTCGATTTCAGGAGGAAATAAAAGA---AAACACAAAAGAACGACAA 540
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RATION NUMBER: 32,172
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51 University Street
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51.9%;
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Pred. No. 1.4e-09;
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Search completed: July 8, 2002, 20:04:42 Job time: $721 \ \text{sec}$

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2: /SIDS5/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*

3: /SIDS5/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*

4: /SIDS5/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:*

5: /SIDS5/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT:*

6: /SIDS5/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT:*

7: /SIDS5/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:*

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/SIDS5/gcgdatta/geneseq/geneseqp-emb1/AA1990.DAT:
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AAWIY//	AAW19787	AAW27134	AAW95032	AAW76332	AAY27017	AAY27016	AAY91020	AAY84426	AAY91023	AAY84425	AAY84424	AAY84423	AAY84422	AAB08272	AAY84421	AAY84420	AAU08386	AAB67248	AAB08273	AAW83019	AAB84420	AAY17873	AAW83020	AAE01992	AAE04425	AAE08737	AAW68292	AAW69956	AAB82092	AAY84419	AAY84418	91	AAY17874
Novel cytokine Apo	apoptosis	Human Apoptosis in		TL2	Apo-2		Mouse OBM protein	An osteoprotegerin	Mouse OBM protein	DNA encoding osteo	An osteoprotegerin	An osteoprotegerin	ine of	acid	acid				Amino acid sequenc			Human TRANCE. Hom	_	RANKL (r	receptor	e receptor a	receptor ac	NF-kB receptor act	steoc1	acid	acid sequ	OBM protei	Murine TRANCE. Mu

ALIGNMENTS

RESULT AAW83195

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AAW83195 standard; Protein;

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11-FEB-1999 AAW83195;

(first entry)

30-MAR-1998; 16-APR-1997; 23-JUN-1997; Human; osteoprotegerin binding protein; OPG binding protein; arthritis; osteoporosis; osteoclast maturation; bone disease; metastasis; ODAR; hypercalcaemia; osteoclast differentiation and activation receptor; Paget's disease. WPI; 1998-594578/50. N-PSDB; AAV70285. Human osteoprotegerin binding protein from the pcDNA/huOPGbp1.1insert. Boyle WJ; (AMGE-) AMGEN 15-APR-1998; 22-OCT-1998. WO9846751-A1 Homo sapiens. INC 98US-0052521. 97US-0842842. 97US-0880855. 98WO-US07584

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RESULT
AAW69957
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is human osteoprotegerin (OPG) binding protein.
CC Host cells transfected with vectors containing nucleic acid molecules canceding OPG binding protein are used to produce recombinant OPG binding protein are used in binding assays to determine osteoprotegrin (OPG) in biological samples; to screen for specific binding agents (particularly agonists and antagonists, including contracellular proteins); to raise Ab (useful in immunoassays for modulate binding of OPG binding protein) and to identify compounds that modulate binding of OPG binding protein to osteoclast differentiation and activation receptor (ODAR). The nucleic acid molecule encoding OPG binding protein can be used to detect OPG binding protein-encoding CC sequences, e.g. screening for related sequences, also to produce transgenic animal models, while complementary sequences are used for antisense regulation of OPG binding protein expression. Modulators of OPG binding protein, particularly soluble forms of OPG binding protein, paget's of options of OPG binding of prostheses, periodontal disease, osteoporosis, hope creates and paget's options of OPG binding of prostheses, options of OPG binding protein of OPG binding protein of OPG binding protein options of OPG binding protein of OPG binding options of OPG binding of OPG binding of OPG binding options of OPG binding 
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                                                             RANK; necrosis factor-kappa B; NF-kB; receptor activator; human; immune response; inflammatory response; toxic shock; sepsis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                             AAW69957;
                                                                                                                                                                                                                                                                       AAW69957 standard; Protein;
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                                                                                                                                 receptor activator RANK ligand (RANKL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               317 AA;
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                                          tumour necrosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CC activator of necrosis factor kappab (NF-kB)) polypeptide. RANK is a CC member of the tumour necrosis factor (TNF) family. A soluble RANK CC may be used for inhibiting activation of NF-kB, by contacting a cell C expressing membrane-associated RANK with a soluble RANK which binds to CC RANK ligand (RANKL). RANKL polypeptides can activate RANK which binds to CC allo-stimulatory capacity, thereby augmenting an immune response. The CC allo-stimulatory capacity, thereby augmenting an immune response. The CC immune or inflammatory response. Inhibition of NF-kB by RANK antagonists CC may be useful in ameliorating negative effects of an inflammatory CC response that result from triggering of RANK, e.g. in treating toxic CC shock or sepsis, graft-versus-host reactions, or acute inflammatory CC reactions. They can also be used in adjunct therapy for disease CC can also be used to identify inhibitors of RANK. RANKL polypeptides CC can also be used for protecting RANK. RANKL polypeptides CC can also be used for protecting RANK. Pospressing cells from the negative effects of chemotherapy or the presence of high levels CC from the negative effects can also be used for protecting RANK-expressing cells cof TNF-alpha. The products can also be used for detection and drug
                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100. Matches 317; Conservative
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23-DEC-1996;
07-MAR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated ligand for receptor activator of NF-kappa develop products for augmenting an immune response for
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N-PSDB; AAV41378.
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                                                                                       KVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240
                                                                                                                                                                                                                                                          VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
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 PDQDATYFGAFKVRDID
                                                              YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD
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96US-0059978.
97US-0813509.
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Pred. No. 2.6e-156;
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                                                                                                                      Matches
                                                                                                                                    Query Match
Best Local :
                                                                                                                                                                                                             activator of necrosis factor kappaB (NF-kB)) polypeptide. FANK is a member of the tumour necrosis factor (TNF) family. Host cells transformed or transfected with an expression vector comprising the RANK encoding nucleic acid can be used to produce recombinant RANK protein. The soluble RANK may be used for inhibiting activation of NF-kB, by contacting a cell expressing membrane-associated RANK with a soluble RANK which binds to RANK ligand (RANKL). The soluble RANK polypeptide composition may also be used for regulating an immune or inflammatory response. Inhibition of NF-kB by RANK antagonists may be useful in ameliorating negative effects of an inflammatory response that result from triggering of RANK, e.g. in treating toxic shock or sepsis, graft-versus-host reactions, or acute inflammatory reactions. They can also be used in adjunct therapy for disease characterised by neoplastic cells that express RANK. The products can also be used for detection and drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-OCT-1997;
23-DEC-1996;
07-MAR-1997;
                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated receptor activator of necrosis factor-kappa B for, e.g. developing products for regulating an immune or inflammatory response, treating toxic shock or sepsis
                                                                                                                                                                                                                                                                                                                                                                                                                    This represents a human RANKL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RANK; necrosis factor-kappa B; NF-kB; receptor activator; human; immune response; inflammatory response; toxic shock; sepsis; RANKL; RANK ligand; tumour necrosis factor; TNF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  7; Pages 59-60;
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                                                                                                                  100.0%;
illarity 100.0%;
Conservative 0
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97US-0813509.
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                                                                                                                               Score 1685; DB 19;
Pred. No. 2.6e-156;
                                                                                                                                                                                                                                                                                                                                                                                                                                             English.
                                                                                                                                                                                                                                                                                                                                                                                                                  a ligand for the RANK (receptor
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The present sequence represents a human osteoprotegerin ligand (OPGL). Osteoprotegerin is a secreted member of the tumour necrosis factor receptor family, which blocks osteoclastogenesis in a dose dependent manner. The OPGL protein is synthesised as a type II transmembrane protein. The murine and human OPGL polypeptides are 87% homologous. OPGL is a potent osteoclast differentiation factor when combined with CSF-1. It is not capable of inducing osteoclast differentiation in the absence of CSF-1. OPGL is also an activator of mature osteoclasts. The specification describes a method for the in vivo down-regulation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Osteoprotegerin ligand; OPGL; osteoprotegerin; osteoclastogenesis; tumour necrosis factor receptor; type II transmembrane protein; osteoclast differentiation; CSF-1; osteoclast activator;
                                                                                                                   Claim
                                                                                                                                                                                                                                                     15-SEP-1998;
02-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                         Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   response; osteoporosis; bone resorption.
                                                                                                                                      down-regulation of osteoprotegerin ligand (OPGL) activity used
t, prevent and ameliorate osteoporosis -
                                                                                                                                                                          AAZ99964.
                                                                                                                Page 78-79; 110pp;
                                                                                                                                                                                                        Haaning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence of a human osteoprotegerin ligand
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                                                                                                                                                                                                                                                                                                                                                                                                  "transmembrane
                                                                                                                                                                                                                                                                                                                                                      "active ligand moiety"
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OPGL activity in an animal. The method comprises using at least one OPGL polypeptide or subsequence, and/or at least one OPGL analogue to induce an immune response in the animal. The method and OPGL polypeptide are useful for treating, preventing and ameliorating osteoporosis or other diseases or conditions characterised by excessive bone resorption.
                                                                               23-DEC-1996;
07-MAR-1997;
14-OCT-1997;
                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                          anti-apoptotic signal;
                                                                                                                                                                                                                                                                                                                                    AAE08738 standard; Protein;
         Dougall
                                                             23-DEC-1996;
07-MAR-1997;
                                                                                                                          17-DEC-1998;
                                                                                                                                                                   US6271349-B1
                                                                                                                                                                                                          immune response; inflammatory response; graft-versus-host reaction;
toxic shock; sepsis; acute inflammatory reaction; bone resorption;
anti-apoptotic signal; therapy; immunosuppressant; anti-inflammatory
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                             ( VMMI)
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317; Conser
                                                                                                                                                                                                                                         receptor activator of nuclear factor kappaB ligand; RANKL; necrosis factor; TNF; TNF receptor associated factor; TRAF;
          WC,
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nilarity 100.
Conservative
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                                                 96US-0772330.
97US-0813509.
97US-0996139.
                                                                                 96US-0059978.
97US-0077181.
97US-0064671.
                                                                                                                                                                                                                                                                         activator of NF kappaB ligand (RANKL) protein
                                                                                                                          98US-0215649
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Pred. No. 2.6e-156;
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WPI; 2001-520313/57.
N-PSDB; AAD15311.
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regulating immune re adjunct therapy for express RANK .-New receptor activator of NF-kappaB (RANK) polypeptides, useful for regulating immune response, in screening for RANK inhibitors, or as adjunct therapy for disease characterized by neoplastic cells that or as an

Example 15; Column 71-72; 47pp; English.

cc are useful for regulating immune response and in screening for inhibitors of signal transduction, e.g. for screening for inhibitors of signal transduction, e.g. for screening the common of real properties and particularly TRAF6. NF-kappaB inhibition by RANK antagonists of are useful in ameliorating the negative effects of an inflammatory cc response that result from triggering of RANK, e.g. in treating twoic cc shock or sepsis, graft-versus-host reactions, acute inflammatory cc reactions and the effects of bone resorption. RANK acts as an antice appropriate signal and rescue the cells that express RANK from apoptosis. Cc Soluble forms of the receptor are used in vivo or in vitro based cc antagonists of RANK-mediated NF-kappa B activation, or to inhibit transduction of a signal via RANK. RANK compositions are used in the adjunct therapy for disease characterised by neoplastic cells that express RANK. Compounds that interfere with RANK/TRAF6 interactions are useful for modulating osteoclast function and activities. They recursors and for modulating osteoclast function and activities. They care used as inhibitors of diseases associated with excess bone resorption and as immunosuppressants or anti-inflammatory agents. The RANK DNAs are useful for the expression of recombinant proteins, as probes for analysis of are useful in preparing kits for the detection of soluble RANK, or analysis of monitor RANK-related activity. The present sequence is RANK ligand cc ranker, are related activity. The present sequence is RANK ligand kappaB (RANK) proteins and their corresponding DNAs. RANK is a member of the tumour necrosis factor (TNF) receptor superfamily and associates with TNF receptor associated factor (TRAF) 2 and 3 which are important in the regulation of immune and inflammatory response. The receptors receptor activator of nuclear factor (NF)-

Sequence

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Matches 317;
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YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD
                                                                                                                                                                                                                                                                                                                                                                                                  KVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV
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Pred. No. 2.6
0; Mismatches
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2.6e-156;
s 0;
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AAE04426
                                                                                                                                                                                                                                                     The present invention relates to receptor activator of NF-chi B (RANK) DNA. RANK is mapped to chromosome 18q22.1 and its ligand (RANKL) to chromosome 13q14. RANK and RANKL are type 1 and type 2 transmembrane proteins respectively. RANK is a member of the tumour necrosis factor (TNF) superfamily and it closely resembles CD40 in the extracellular region. RANK associates with TNF receptor-associated factor (TRAF) 2 and TRAF3. The DNA molecules are useful for producing ligands of RANK. The ligands are useful for regulating immune response and in screening for inhibitors of RANK. The present sequence is human RANKL (hurankkl)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-DEC-1996;
07-MAR-1997;
14-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                           New DNA molecules, useful for producing ligands (which are useful for regulating immune response and in screening for inhibitors of NF-chi B receptor activator) of the receptor activator of NF-chi B (RANK) -
                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Key
Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; receptor activator of NF-chi B; RANK; tumour necrosis factor; CD40; TNF receptor-associated factor; TRAF; ligand; immune response; chromosome 18q22.1; huRANKL; chromosome 13q14; transmembrane protein.
                                                                                                                                                                                                                                                                                                                                                                                         Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JUN-2001.
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                                                                                                                                                         Local Similarity
nes 317; Conserv
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                                                                VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
                                                                                                  vcsvalffyfraqmdpnrisedgthclyrilrlhenadfqdttlesqdtklipdscrrik 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAD08715
                                                                                                                                                                                                                                                                                                                                                                                     Column 65-66; 43pp; English.
                                                                                                                                                                                                                        317 AA;
                                                                                                                                                      100.0%; ilarity 100.0%; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96US-0059978.
97US-0077181.
97US-0064671.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97US-0995659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Receptor binding region"
                                                                                                                                                        <u>,,</u>
                                                                                                                                                      Score 1685; DB 22;
Pred. No. 2.6e-156;
Mismatches 0;
                                                                                                                                                                                DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (huRANKL)
                                                                                                                                                        Indels
                                                                                                                                                                              Length 317;
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AAE01993
The present invention relates to a novel receptor, referred to as RANK CC (receptor activator of NF (nuclear factor)-kappaB), a member of TNF CC (tumour necrosis factor) receptor superfamily. RANK is a Type I CC transmembrane protein that interacts with TNF receptor-associated CC factors (TRAFS). Triggering of RANK by overexpression or co-expression CC of RANK and membrane bound RANK ligand (RANK) results in upregulation CC of the transcription factor NF-kappaB, a ubiquitous transcription factor CC that is most extensively utilised in cells of the immune system. CC Inhibition of NF-kappaB by RANK antagonists is useful in ammeliorating negative effects of inflammatory reactions, and the effects of excess come resorption. The RANK DNAs, proteins and their analogues are useful CC to the preparation of pharmaceutical compositions, for infecting target cells for use in gene therapy applications in diagnosing diseases associated with RANK, and as targets for use in screening assays. They may be used in the treatment or diagnosis of immune system dysfunction. The present invention also encompasses gene therapy methods to correct contently and early onset Paget's disease of bone (EP). The present amino acid sequence is full-length human RANKL (huRANKL) correct content in the content of the content 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 76-77; 96pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New DNA encoding a receptor activator of NF-kappaB polypeptide for the treatment of Paget's disease and Familial Expansile Osteolysis (FEO) -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB;
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SX XX

Sequence

317

A

Query Match Best Local S Matches 317

al Similarity 317; Conserv

Conservative

0;

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Indels Length

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Gaps

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100.0%;

Score 1685; DB 22; Pred. No. 2.6e-156; Mismatches

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AAW83018
ID AAW8
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15-APR-1997;
09-JUN-1997;
12-AUG-1997;
21-AUG-1997;
                                                                                                                                                                                                                          Goto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           osteoclast; bone absorption factor; bone disorder; calcium metabolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Osteoclastogenesis inhibitory factor (OCIF)-binding molecule (OBM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW83018 standard; Protein;
calcium metabolism
                       protein binding to osteoclastogenesis inhibitory factor - useful
for, e.g. treatment and investigation of disorders of bone and
                                                                                                 WPI; 1998-594563/50
N-PSDB; AAV69887.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Osteoclastogenesis inhibitory factor; OCIF; OCIF-binding
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N, Shima N,
                                                                                                                                                                           Yamaguchi
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97JP-0097808.
97JP-0151434.
97JP-0217897.
97JP-0224803.
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                                                                                                                                                                                                   Kinosaki M,
Takahashi K,
                                                                                                                                                                           Yano K,
                                                                                                                                                                                                                          Kobayashi
                                                                                                                                                                           Yasuda
                                                                                                                                                                           Tomoyasu
Yasuda H;
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                                                                                                                                                                                                   Morinaga
Tsuda E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           molecule;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  function and calcium of the protein, for components of drugs.
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(OCIF)-binding
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                                                                                                                                                                                                                                  hypercalcaemia;
Paget's disease.
                                                                                                                                                                                                                                                                                    Human; osteoprotegerin binding protein; OPG binding protein; as osteoporosis; osteoclast maturation; bone disease; metastasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW83194;
                         15-APR-1998;
                                                                                                                                W09846751-A1
                                                                                                                                                                                     Homo
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                                                                           22-OCT-1998
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Local 5
316;
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                                                                                                                                                                                                                                                                                                                                                                        osteoprotegerin
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ing molecule (OBM). '
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                           98WO-US07584.
                                                                                                                                                                                                                                                                   osteoclast differentiation and
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99.7%;
                                                                                                                                                                                                                                                                                                                                                                        binding
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Pred. No. 1.6e-155;
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                                                                                                                                                                                                                                                                                                                                                                             from the
                                                                                                                                                                                                                                                                         activation receptor;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local :
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16-APR-1997;
23-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid encoding osteoprotegrin binding protein - useful for, e.g. treating bone diseases by modulating osteoclast differentiation and for diagnosis
                  AAW83017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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N-PSDB; AAV70284.
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                                                                                                        DPDQDATYFGAFKVRDID
                                                                                                                                                KOAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGS
                                                                                                                                                                                                                                                                                                                                vvcsialflyfraqmdpnrisedsthcfyrilrlhenaglqdstlesedt--lpdscrrm 118
                                                                                                                                                                                                                                                                                                                                                 VVCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRI 119
                                                                                           dpdqdatyfgafkvqdid
                                                                                                                                                                                                                                                                                                                                                                                           mrrasrdygkylrsseemgsgpgvphegplhpapsapapapppaasrsmflallglglgq
                                                                                                                                                                                                                                                                      kqafqgavqkelqh1vgpqrfsgapammegswldvaqrgkpeaqpfahltinaasipsgs
                  standard;
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97US-0842842.
97US-0880855.
                  Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84.1%;
                                                                                                                       317
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                  316
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Pred. No. 3.8e-1
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 19;
e-130;
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Query Match
Best Local :
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12-AUG-1997;
21-AUG-1997;
                                                                                                                                                                                                                                                                                                                                         The present sequence represents an osteoclastogenesis inhibitory factor (OCIF)-binding molecule (OBM). The protein promotes and supports the separation and maturation of osteoclasts in the presence of bone absorption factors such as calcitriol or parathyroid hormone (PTH). OBM is isolated from stroma cells cultured in the presence of a bone absorption factor by separation and solubilisation of membrane proteins then affinity chromatography using OCIF. It exists in a full-sequence form and a solubilised form (SOBM) which is a shorter chain. OBM may be used for screening potential inhibitors and modifiers of its biological activity, and screening for receptors to OBM which mediate its function. These substances can then be used in the treatment of disorders of bone function and calcium metabolism. The antibodies can be used for assay of the protein, for investigative and diagnostic purposes, and as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein binding to osteoclastogenesis inhibitory factor - useful for, e.g. treatment and investigation of disorders of bone and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Osteoclastogenesis inhibitory factor; OCI osteoclast; bone absorption factor; bone
                                                                                                                                                                                                                                                                                                  Sequence
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15-APR-1997;
                                                                                                                                                                                                                                                                                                                                 components
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                                119
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                                                                                                                                                                       1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLH-APPPPAPHQPPAASRSMFVALLGLGLGQ
                                                                                                         VVCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRI 119
HKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLM
                                           KQAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGS
                                                                                          vvcsialflyfraqmdpnrisedsthcfyrilrlhenaglqdstlesedt--lpdscrrm
                                                                                                                                                     {\tt mrrasrdygkylrsseemgsgpgvphegplhpapsapapapapapasrsmflallglglgq}
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                             kqafqgavqkelqhivgpqrfsgapammegswldvaqrgkpeaqpfahltinaasipsgs
                                                                                                                                                                                                                       268;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8; Pages 106-108; 151pp; Japanese.
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                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   metabolism
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a N, Shima N,
N, Yamaguchi
                                                                                                                                                                                                                                                                                                                               of drugs.
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97JP-0097808.
97JP-0151434.
97JP-0217897.
97JP-0224803.
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Takahashi K, Tomoyasu
K, Yano K, Yasuda H;
                                                                                                                                                                                                                      16;
                                                                                                                                                                                                                                 Score 1417.5;
Pred. No. 3.8e
                                                                                                                                                                                                                      Mismatches
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Length 316;

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                                                            lupus erythematosus, Hashimoto's autoimmune thyroiditis, as well as acute inflammatory responses in which T-cell expansion, activation or immunological T-cell memory play an important role. The antibodies can be used to raise anti-idiotypic antibodies which will be useful in detecting or diagnosing various immunological conditions related to the expression of antigens of 499E9. The antibodies, and fragments of the expression of antigens of 499E9.
                                                                                                                                         This is the amino acid sequence of the mouse 499E9 protein, used in the method of the invention to treat conditions associated with abnormal physiology or development. The 499E9 protein is expressed highly on polarised Th1 T cells, binding of 49E9 to its receptor may result in either immune cell expansion or apoptosis. Antagonists of 49E9 may be used to modulate immune responses in abnormal situations, e.g. autoimmune disorders including rheumatoid arthritis, systemic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Domain
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systemic lu
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                                                                                                                                                                                                                                                  Claim 1;
                                                                                                                                                                                                                                                                                        Mouse cell
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Sequence
                                    abnormal
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                                   n be used in the treatment of conditions associated with physiology or development, including abnormal prolifera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lupus
                                                                                                                                                                                                                                                                        with abnormal physiology or dev
316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     autoimmune disorder; rheumatoid arthritis;
pus erythematosus; Hashimoto's autoimmune thyroiditis;
mmatory response; antibody; antigen; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein;
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                          conditions) or
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                          including abnormal proliferation
nerative conditions.
                                                  The antibodies, and fragments of conditions associated with
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Best Local S
Matches 268
                                                                                                                                                                                         11-DEC-1998;
12-DEC-1997;
03-MAR-1998;
        The present sequence represents murine TNF-related activation induced cytokines (TRANCE). Human or murine TRANCE polypeptides or their variants, fragments, derivatives or analogues may be used as modulators of immune response in a mammal comprising, antisense sequences to
                                                                                                                                              Choi
                                                                                                                                                                                                                                                                                                                          TRANCE; tumour necrosis factor superfamily; signal transduction; TNF-related activation induced cytokine; immune response; cancer; autoimmune disease; HIV; hypersensitivity; allergen.
                                                                                                             WPI; 1999-385609/32.
N-PSDB; AAX80224.
                                                                                                                                                                                                                                                            17-JUN-1999
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                                                                                                                                                                                                                                                                                                       Mus musculus
                                                                                                                                                                                                                                                                                                                                                                        Murine TRANCE
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                                                                 Claim
                                                                                        TNF like
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97US-0989479.
98US-0034099.
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Pred. No. 3.8
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                                                                                        autoimmunity and
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Example

1; Page 15-16; 18pp; Japanese

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                                                                                                                                  (SNOW)
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A DNA and preparation
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N-PSDB; AAA39156.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     osteoclastogenesis inhibitory factor binding molecule; steoclast; bone absorption promoting factor; vitamin D3;
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84.3%; Pred. No. 3.8e-130;
tive 16; Mismatches 31; I
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes a genomic DNA encoding a protein having an activity of supporting or promoting differentiation and maturation of osteoclasts. The genomic DNA encoding a protein has the following properties: (a) combines specifically with osteoclastogenesis inhibitory factor (OCIF) and has a high affinity; (b) shows a molecular weight (mw) of 30,000 to 40,000 by SDS-PAGE (sodium dodecyl sulfate-polyacrylamide gel electrophoresis) under a nonreductive condition and the apparent mw when crosslinked with monomer type OCIF is 90,000 to 110,000; and (c) has an activity of supporting or promoting differentiation and maturation of osteoclast in the co-culture of mouse osteoblast-like stroma cell and mouse spleen cell in the presence of a bone absorption promoting factor such as active type vitamin D3 and parathyroid hormone (PTH). The protein can be used as a drug and a research reagent. The present sequence inventors a mouse OCIF binding molecule (OBM) from the present
               Domain
                                       Domain
                                                                                                            tumour necrosis factor receptor; type II transmembrane prosteoclast differentiation; CSF-1; osteoclast activator; immune response; osteoporosis; bone resorption.
                                                                                                                                                         Osteoprotegerin ligand; OPGL; osteoprotegerin; osteoclastogenesis;
                                                                                                                                                                                                                                                AAY84418
                                                                                                                                                                                                                                                                               AAY84418 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                  Mus musculus
                                                                                                                                                                                      Amino acid sequence of a murine osteoprotegerin ligand (OPGL).
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          /note= "transmembrane 70..157
                                       Location/Qualifiers 48..71
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84.3%; Pred. No. 3.8e-130;
tive 16; Mismatches 31;
"extracellular stalk domain"
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                             domain"
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Matches
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                                                             DPDQDATYFGAFKVRDID
                                                                                                                                              mrrasrdygkylrsseemgsgpgvphegplhpapsapappppaasrsmflallglglgg 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             down-regulation of osteoprotegerin ligand (OPGL) activity used t, prevent and ameliorate osteoporosis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Page 81-82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              316
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Qy

Query Match
Best Local Similarity

84.1%;

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Indels Length

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Matches

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RESULT 15
AAY84419
manner. The OPGL protein is synthesised as a type II transmembrane protein. The murine and human OPGL polypeptides are 87% homologous. OPGL is a potent osteoclast differentiation factor when combined with CSF-1. It is not capable of inducing osteoclast differentiation in the absence of CSF-1. OPGL is also an activator of mature osteoclasts. The specification describes a method for the in vivo down-regulation of OPGL activity in an animal. The method comprises using at least one OPGL polypeptide or subsequence, and/or at least one OPGL analogue to induce an immune response in the animal. The method and OPGL polypeptide are useful for treating, preventing and ameliorating osteoporosis or other useful control of the con
                                                                                                                                                                                                                                                                                                                     The present sequence represents a murine osteoprotegerin ligand (OPGI Osteoprotegerin is a secreted member of the tumour necrosis factor receptor family, which blocks osteoclastogenesis in a dose dependent
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                                                 or conditions
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/cgn2_6/ptodata/2/1aa/6A_COMB.pep:*
/cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
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9.4	9.4	9.4	9.4	9.4	9.4	9.4	9.8		10.4	10.9	10.9	10.9	11.2	11.2	11.2	11.2	11.2
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Sequence 12, Ap	Sequence 2, Appl	Sequence 4, Appl	Sequence 4, Appl.	Sequence 2, Appl	Θ,	Sequence 2, App	Sequence 8, App	26,	Sequence 16, A	5	•	Sequence 24, App	Sequence 2, Appl	ŗ	Sequence 8, App	Sequence 3, App	Sequence 25, A
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ALIGNMENTS

; MOLECULE TYPE: US-08-996-139-13 RESULT 1 US-08-996-139-13 Sequence 13, Application US/08996139 Patent No. 6017729 TELEFAX: (206)233-064
INFORMATION FOR SEQ ID NO: FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-/
TELECOMMUNICATION INFORMATION: GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operation SEQUENCE CHARACTERISTICS: LENGTH: 317 amino acids TYPE: amino acid PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/064,671
FILING DATE: 14 OCTOBER 1997
PRIOR APPLICATION DATA: SOFTWARE: Microsoft WO CURRENT APPLICATION DATA: TITLE OF INVENTION: Receptor Activator of NF-kappaB NUMBER OF SEQUENCES: 19 CORRESPONDENCE ADDRESS: APPLICATION NUMBER: FILING DATE: 22 DECCLASSIFICATION: STATE: V TELEPHONE: TYPE: amino acid TOPOLOGY: linear ADDRESSEE: 98101 Seattle ΜA E: Immunex Corporation, Law Department 51 University Street (206)233-0644 USA (206)587-0430 protein 22 DECEMBER 1997 Apple Operating System 7.5. ft Word for Power Macintosh US/08/996,139 2851-A System 7.5.5 Macintosh 6.0.1

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US-08-995-659-13
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Best Local Similarity
Matches 317; Conserv
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MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
COMPUTER: Apple Power Macintosh
COMPUTER: Apple Operating System 7.5.5
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.9
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/995,659
FILING DATE: 22 DECEMBER 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                  ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION UNMBER: 34,693
REFERENCE/DOCKET NUMBER: 2857
                                                                                                                                                                                              FILING DATE: 14 OCTOBER 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
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CITY: Seattle
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                                                                                                                                                                           FILING DATE: 0
CLASSIFICATION:
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                                                                                               CLASSIFICATION:
                                                                                                           APPLICATION NUMBER: USSN STILING DATE: 23 DECEMBER
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INFORMATION:
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                                                                                                                   USSN 08/772,330
EMBER 1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 13, Application US/09215649A; Patent No. 6271349; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 3
US-09-215-649A-13
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Best Local Similarity 100.0%;
Matches 317; Conservative 0
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                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.
SOFTWARE: Microsoft Word for Power Macintosh
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                         Galibert, Laurent
Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
                                                                                                       APPLICATION NUMBER: US/09/215,649A FILING DATE: 17-Dec-1998 CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                       ZIP: 98101
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Anderson, Dirk M
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                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Immunex Corporation, Law Department STREET: 51 University Street
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
                                                                      APPLICATION NUMBER: 08/996,139 FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                            CITY: Seattle
                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                           STATE: WA
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(206)233-0644
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Pred. No. 9.8e-164;
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FILE REFERENCE: A-451Brv

CURRENT APPLICATION NUMBER: US/09/052,521C

CURRENT FILING DATE: 1998-03-30

PRIOR APPLICATION NUMBER: 08/880,855

PRIOR FILING DATE: 1997-06-23

PRIOR APPLICATION NUMBER: 08/842,842

PRIOR FILING DATE: 1997-04-16

NUMBER OF SEQ ID NOS: 40

SOFTWARE: PATENTIN Ver: 2.1
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                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/09052521C Patent No. 6316408 GENERAL INFORMATION:
   Query Match
Best Local Similarity
Matches 317; Conserv
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Best Local
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TITLE OF INVENTION: Osteoprotegerin Binding Proteins and Receptors
                                                                                             LENGTH: 317
TYPE: PRT
ORGANISM: Human
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Local Similarity 100.0%;
hes 317; Conservative (
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TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION: NAME: Perkins, Patrici
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REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 317 amino acids
   Conservative
             100.0%; Score 1685; DB 4; 100.0%; Pred. No. 9.8e-164;
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Pred. No. 9.8e-164;
; Mismatches 0;
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                                                                                                       Query Match
Best Local Similarity 84.3
Matches 268; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 316 amino acid
                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION: NAME: Winter, Robert B.
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TITLE OF INVENTION: OSTEOPROTEGERIN BINDING PROTEINS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
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ZIP: 912
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CITY: Thousand Oaks
STATE: California
  61
             60 VVCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRI 119
                                                                                                                                                                                                                 TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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VVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESEDT--LPDSCRRM
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                                                                                                                             84.1%;
84.3%;
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                                                                                                                16;
                                                                                                             Score 1417.5;
Pred. No. 1.9e
16; Mismatches
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                                                                                                             .5; DB 2;
1.9e-136;
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                                                                                                                               Query Match 84.1%; Score 1417.5; DB 4
Best Local Similarity 84.3%; Pred. No. 1.9e-136;
Matches 268; Conservative 16; Mismatches 31;
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                                                                                                                                                                                                                                                                                                                    TELEFAX: (650)496-1204 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/989,362
FILING DATE: 12-DEC-1997
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CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Gorman, Daniel M.
APPLICANT: Mattson, Jeanine D.
TITLE OF INVENTION: Mammalian Cell Surface Antigens; Related
TITLE OF INVENTION: Reagents
                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 316 amino acid
                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: (650)852-9196
                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 13-DEC-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 56
PRIOR APPLICATION DATA:
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CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                      NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0686
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 60/032,846 FILING DATE: 13-DEC-1996
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                 VVCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRI 119
                                                                  MRRASRDYGKYLRSSEEMGSGPGVPHEGPLHPAPSAPAPAPPPAASRSMFLALLGLGLGQ 60
                                                                                    MRRASRDYTKYLRGSEEMGGGPGAPHEGPLH-APPPPAPHQPPAASRSMFVALLGLGLGQ
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PRIOR FILING DATE: 1997-06-23;
PRIOR APPLICATION NUMBER: 08/84;
PRIOR APPLICATION NUMBER: 1997-04-16;
PRIOR FILING DATE: 1997-04-16;
NUMBER OF SEQ ID NOS: 40;
SOOTWARE: Patentin Ver. 2.1;
SEQ ID NO 2;
LENGTH: 316;
TYPE: PRI ORGANISM: Mouse
US-09-052-521C-2
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Best Local Similarity
Matches 268; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Boyle, William J.
TITLE OF INVENTION: Osteopro
FILE REFERENCE: A-451Brv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/052,521C CURRENT FILING DATE: 1998-03-30 PRIOR APPLICATION NUMBER: 08/880,855 PRIOR FILING DATE: 1997-06-23
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                                                                                                               VYVVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLL
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Sequence

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Application

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Patent No. 6017729 GENERAL INFORMATION:

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APPLICATION UMBER: USSN 08/813, FILING DATE: 07 MARCH 1997 PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/772, APPLICATION NUMBER: USSN 08/772, APPLICATION NUMBER: USSN 08/772, APPLICATION NUMBER: 1996 ATTORNEY/AGENT INFORMATION:
NAME: PETKINS, PALTICLA ANNE REGISTRATION NUMBER: 34,693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
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COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
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APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
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   239
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CITY: S
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CLASSIFICATION:
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AEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSHKVSLSSWYHDRGWAKISNMTF
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                                 KYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLDPDQDATYFGAFKVRDID 317
                                                                                                                                          GAPAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHKVTLSSWYHDRGWAKISNMTL 178
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US-08-995-659-11
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Best Local Sin
Matches 250;
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Patent No. 624221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Perkins, Patricia Anno
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 281
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
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APPLICATION NUMBER: USSN 60/064,671
FILING DATE: 14 OCTOBER 1997
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APPLICATION NUMBER: US
FILING DATE: 07 MARCH
CLASSIFICATION:
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                                                          202 SNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMVYVTKTSIKIPSSHTLMKGGST 261
                                                                                                                                                                                        COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating S
SOFTWARE: Microsoft Word for Power
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                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
TOPOLOGY: linear
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Galibert,
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                                                                                                                                                                                                                                                      78.7%; Score 1326.5; DB 4; 84.5%; Pred. No. 3.2e-127; tive 16; Mismatches 27;
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; TOPOLOGY: linear; MOLECULE TYPE: protein; SEQUENCE DESCRIPTION: SEQ ID NO: US-09-215-649A-11
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; Sequence 11, Application
; Patent No. 6271349
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Matches 250;
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  202
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                                                                 142 AEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSHKVSLSSWYHDRGWAKISNMTF 201
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                                                                                                                                                                                                                         23 GAPHEGPLH-APPPPAPHQPPAASRSMFVALLGLGLGQVVCSVALFFYFRAQMDPNRISE 81
                                                                                                                                                                                                                                                                                                           Local Similarity
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FILING DATE: <Unknown>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
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Galibert, Laurent
Maraskovsky, Eugene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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  SNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMVYVTKTSIKIPSSHTLMKGGST
                                        GAPAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHKVTLSSWYHDRGWAKISNMTL 178
                                                                                                                        DSTHCFYRILRLHENADLQDSTLESEDT - - LPDSCRRMKQAFQGAVQKELQHIVGPQRFS 118
                                                                                                                                                           DGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIKQAFQGAVQKELQHIVGSQHIR 141
                                                                                                                                                                                                      GVPHEGPLHPAPSAPAPPPPAASRSMFLALLGLGLGQVVCSIALFLYFRAQMDPNRISE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/215,649A FILING DATE: 17-Dec-1998 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Immunex Corporation, STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 294 amino acids TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                      Conservative
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84.5%;
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                                                                                                                                                                                                                                                                                    16;
                                                                                                                                                                                                                                                                                                         Score 1326.5; DB 4;
Pred. No. 3.2e-127;
                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                            11:
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US-08-670-354-2

Sequence 2, Application US/08670354

Patent NO. 5/63223

; GENERAL INFORMATION:
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; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-072-993C-3
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US-09-072-993C-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/056,980 PRIOR FILING DATE: 1997-08-26 PRIOR APPLICATION NUMBER: 60/057,550 PRIOR FILING DATE: 1997-08-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: GH-50030
CURRENT APPLICATION NUMBER: US/09/072,993C
CURRENT FILING DATE: 1998-05-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: A METHOD OF IDENTIFYING AGONIST TITLE OF INVENTION: ANTAGONISTS FOR TUMOR NECROSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Michael R. APPLICANT: Peter R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/055,513
PRIOR FILING DATE: 1997-08-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 9
                                                   APPLICANT: Steven R. Wiley and APPLICANT: Raymond G. Goodwin. TITLE OF INVENTION: Cytokine That NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      179
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                                                                                                                                                                                                                                                                                                   225 RNSCMSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 278
                                                                                                                                                                                                                                                                                                                                      260 STKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLDPDQDATYFGAFKV 313
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                 STREET:
                                    ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -DSYWDPNDEESMNSPCWQVKW------QLRQLVRKMILRTSEETI-----STVQEKQ 105
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Seattle
                 E: Kathryn A. Anderson,
51 University Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14.9%; Score 251.5; DB 4; 24.1%; Pred. No. 1.4e-17; tive 61; Mismatches 117;
                                                                                                    Induces
                                        Immunex Corporation
                                                                                                  Apoptosis
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RELATED RECEPTORS
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STATE: V

RY: WA 98101

USA

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RESULT 13
US-08-584-031-1
US-08-584-031-1
Sequence 1, Application US/08584031A
Sequence 1, Application US/08584031A
Sequence 1, Application US/08584031A
Sequence 1, Application US/08584031A
Sequence 1, Application US/08/584,031A
CURRENT APPLICATION NUMBER: US/08/584,031A
CURRENT FILING DATE: 1996-01-09
NUMBER OF SEQ ID NOS: 17
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OPERATING SYSTEM: Apple 7.5.2
SOFTWARE: MICROSOFT WORD, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/670,354
FILING DATE: 25-JUN-1996
CLASSIFICATION DATA:
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
OR OPPLICATION DATA:
OR OPPLICATION DATA:
OR OPPLICATION DATA:
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REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2835-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 29-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/548,368
FILING DATE: 01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: amino acid
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                      168 HLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYT-SYPDPILLMKSA
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TELEFAX: 756822
                                                                                                                                                                                                                                                                                                                                227 RNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      160 LEAOPF-----AHLT-----INATDIPSGSHKVSL----SSWYHDR-GWAKISNM 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (200) 233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 PSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACF----LKED--- 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/496,632
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QDTTLESQDTKLIPDSCRRIKQAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSK 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  *DSYWDPNDEESMNSPCWQVKW------QLRQLVRKMILRTSEETI-----STVQEKQ 107
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TOPOLOGY:
US-08-780-496-1
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US-08-780-496-1
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-584-031-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08780496 Patent No. 6046048 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 14.9
Best Local Similarity 24.1
Matches 71; Conservative
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                                                                                        TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/
FILING DATE: 08-Jan-197
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MAYSCHAP, Diane L.
                                                                                                                                                    REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5416
                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inch, 1.44 mb floppy disk
                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Avi Ashkenazi, Anan Chuntharapai, Kyung Jin TITLE OF INVENTION: Apo-2 Ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             260 STKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLDPDQDATYFGAFKV 313
                               LENGTH: 281 amin
TYPE: Amino Acid
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                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                  TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                       SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 PSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACF----LKED---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
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08-Jan-1997
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US-08-883-086-10
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US-08-883-086-10
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Best Local :
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Patent No. 6171787
GENERAL INFORMATION:
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Query Match
Best Local Similarity
                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: MEMBER OF THE TNF
TITLE OF INVENTION: FOR TREATMENT AND
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                        NAME: POTEMBER, Priscilla E. REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 6134
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-937-0378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA
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MEDIUM TYPE: Diskette
                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION: NAME: Porembski, Priscil
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
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; Pred. No. 1.4e-17;
61; Mismatches 117;
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   Score 251.5; DB 4;
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DIAGNOSIS OF DISEASE
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CA11_CANFA	SN_MOUSE	V2A_CMVAS	V2A_CMVNT	YK22_YEAST	TNFB_HUMAN	TNFA_TRIVU	V2A_CMVK	CA11_HUMAN	TNFB_MACEU	TNFA_MACEU	TNFC_HUMAN
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P48023

8 h tumor nec 5 m tumor nec 1 homo sapien 2 mus musculu 3 homo sapien 7 mus musculu 9 bos taurus 6 rattus norv 5 homo sapien 5 felis silve 5 cavia porce 6 canis famil 4 mus musculu 4 oryctolagus 3 ovis aries 7 macaca fasc

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TN11_HUMAN
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TN10_HUMAN
TN10_HUMAN
FASL_MUSE
TNF5_BOVIN
FASL_FELCA
TNF5_HUMAN
TNF5_FELCA
TNFA_MOUSE
TNFA_MOUSE
TNFA_HUMAN
TNFA_CANFA
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TNFA_CANFA
TNFA_HORSE
TNFA_BOVIN
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P5114047 P5116940 P36940 P51435 P51435 P51435 P733383 P733383 P73557 P41155 P733383 P736939 P7369 P736

7 homo sapien
2 canis famil
5 homo sapien
4 macaca mula
9 peromyscus
9 rattus norv
5 mus musculu
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4 marmota mund
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InterPro; IPR000478;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: OSTEOCLAST DIFFERENTIATION AND ACTIVATION FACTOR.
AGGMENTS ABILITY OF DENDRITIC CELLS TO STIMULATE NAIVE T-CELL
PROLIFERATION, MAY BE AN IMPORTANT REGULATOR OF INTERACTIONS
BETWEEN T CELLS AND DENDRITIC CELLS AND MAY PLAY A ROLE IN THE
REGULATION OF THE T CELL-DEPENDENT IMMUNE RESPONSE. MAY ALSO PLAY
AN IMPORTANT ROLE IN ENHANCED BONE-RESORPTION IN HUMORAL
HYPERCALCEMIA OF MALIGNARCY.
SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (ISOFORM 1) AND
SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (ISOFORM 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: HIGHEST IN THE PERIPHERAL LYMPH NODES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SECRETED (ISOFORM 2).
ALTERNATIVE PRODUCTS:
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                                                                                                                                                                                                                                                                                                                  MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPPPAPHQPPAASRSMFVALLGLGLGQV 60
                                                                                                                                                          QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH
                    YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD
                                                           KVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV
                                                                              KVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV
                                                                                                                                       QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH
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                                                                                                                                                                                                                                                                                                MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPPAPHQPPAASRSMFVALLGLGLGQV
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al Similarity
317; Conser
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N-LINKED (GLCNAC. .) (F
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A -> G (IN REF. 3).
766176446348097F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                              Score 1685; DB 1;
Pred. No. 7.4e-136;
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                                                                   SEQUENCE
Ikeda T.;
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[3]
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MEDLINE=97460112; PubMed=9312132;
Wong B.R., Rho J., Arron J., Robinson
Kalachikov S., Cayani E., Bartlett F.S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TNFSF11 OR RANKL OR TRANCE OR
                                                                                                                                                      and
                                                                                                                                                                                                                                                                                                                                                                     osteoprotegerin/osteoclastogenesis-inhibitory factor to {\tt TRANCE/RANKL."};
                                                                                                                                                                                                                                                                                                                                                                                                           Yasuda H., Shima N., Nakagawa N., Yamaguchi K., Kinosaki Mochizuki S.-I., Tomoyasu A., Yano K., Goto M., Murakami Morinaga T., Higashio K., Udagawa N., Takahashi N., Suda "Osteoclast differentiation factor is a ligand for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Bone marrow stroma;
MEDLINE=98188248; PubMed=9520411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         differentiation and a Cell 93:165-176(1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Bone marrow;
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                                                                                                                                                                                                 Galibert L.;
                                                                                                                                                                                                                 TISSUE-Thymic lymphoma;
MEDLINE-98032977; PubMed-9367155;
Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.
Tometsko M.E., Roux E.R., Teepe M.C., DuBose R.F., Cosman D
                                                                                                                                                                                                                                                                                                        SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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T., Elliott R., Colombero A., Elliott G., Scully S., Hsu
T., Hawkins N., Davy E., Capparelli C., Eli A., Qian Y.
S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chem.
                                                                                       FROM
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(JAN-2000) to the EMBL/GenBank/DDBJ databases. ION: OSTEOCLAST DIFFERENTIATION AND ACTIVATION FACTOR NTS ABILITY OF DENDRITIC CELLS TO STIMULATE NAIVE T-C
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272:25190-25194(1997).
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.S. III, Frankel W.N., I
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in T cells.";
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EMBL; AF013170; AAC71061.1; --
EMBL; AB008426; BAA25425.1; --
EMBL; AF019048; AAB86812.1; --
EMBL; AF019048; BAA97259.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for come entities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
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VYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNDSLL
                                                                 HKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLM
|||:||||||||| : |:|||||
|KVTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLM
                                                                                                                                                                                                                                                                                                                                                                           MRRASRDYTKYLRGSEEMGGGPGAPHEGPLH-APPPPAPHQPPAASRSMEVALLGLGLGQ
                                                                                                                                                                                    KQAFQGAVQKELQHIYGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGS
                                                                                                                                                                                                                                                     VVCSIALFLYERAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESEDT--LPDSCRRM
                                                                                                                                                                                                                                                                                VVCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRI 119
                                                                                                                                                                                                                                                                                                                                              MRRASRDYGKYLRSSEEMGSGPGVPHEGPLHPAPSAPAPAPPPAASRSMFLALLGLGLGQ
                                                                                                                                                              KQAFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dlfferentlation; Receptor; Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70
197
262
99
316
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84.38;
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SIGNAL-ANCHOR (TYPE II MEMBRANE PROT
(POTENTIAL).

EXTRACELLULAR (POTENTIAL).

N-LINKED (GICNAC. . .) (POTENTIAL).

N-LINKED (GICNAC. . .) (POTENTIAL).

G -> D (IN REF. 4).

G -> D (IN REF. 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1417.5; DB
Pred. No. 3.9e-11
5; Mismatches 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL).
OR (TYPE II MEMBRANE PROTEIN)
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9-113;
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MBL outstation -
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RESULT

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                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Structure of the TRAIL-DR5 complex reveals mechanisms conferring specificity in apoptotic initiation."; Nat. Struct. Biol. 6:1048-1053(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-20017054; PubMed-10549288; Hymowlitz S.G., Christinger H.W., Fuh G. Kelley R.F., Ashkenazi A., de Vos A.M. "Triggering cell death: the crystal st complex with death receptor 5.";
                   EMBL; U37518; AAC50332.1; EMBL; U57059; AAB01233.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TN10_HUMAN P50591;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jonés E.Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=10542098;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mongkolsapaya J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         K-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 119-281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mol. Cell 4:563-571(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=96278649; PubMed=8663110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-96111955; PubMed-8777713; Wiley S.R., Schooley K., Smolak P.J., Din wicholl J.K., Sutherland G.R., Davis-Smith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-1996 (Rel. 34,
01-OCT-1996 (Rel. 34,
01-MAR-2002 (Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Induction of apoptosis by Apo-2 ligand, necrosis factor cytokine family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ashkenazi A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pitti R.M., Marsters
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunity 3:673-682(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               crosis factor cytokine family.";
Biol. Chem. 271:12687-12690(1996).
                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: HOMOTRIMER (POTENTIAL).
SUBCELLULAR LOCATION: Type II membrane protein (Potential).
TISSUE SPECIFICITY: WIDESPREAD; MOST PREDOMINANT IN SPLEEN,
                                                                                                                                                                                                                                                                                                                      SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: INDUCES APOPTOSIS
                                                                                                                                                                                                                                                                                                                                                  AND PROSTATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Screaton G.R.;
                                                                                                                                                                                                                                                                                                                BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J.M., Chen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     new member of the tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of Apo2L/TRAIL in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stuart D.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Moore A.,
                                                                                                                                                                                                                                    collaboration -
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RESULT 4
TN10_MOUSE
ID TN10_M
AC P50592
DT 01-CT
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SEQUENCE
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PROSITE; PS00251; TNF_1; 1.

PROSITE; PS50049; TNF_2; 1.

CYTOKINE; Transmembrane; Signal-anchor; Apoptosis; 3I

CYTOKINE; Transmembrane; CYTOPLASMIC (POTENTIAL)
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InterPro; IPR003636; TNF_abc.
InterPro; IPR000478; TNF_family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ProDom; PD002012; TNF_abc; 1. ProDom; PD008600; TNF_5; 1.
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PDB; 1D4V; 01-NOV-99.
                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

MEDLINE-96111955; PubMed-8777713;

Wiley S.R., Schooley K., Smolak P.J., Din W.S.,

Nicholl J.K., Sutherland G.R., Davis-Smith T., I

Goodwin R.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TN10_MOUSE STANDARD; PRT; 291 AA. p50592; 01-0CT-1996 (Rel. 34, Created) 01-0CT-1996 (Rel. 34, Last sequence update) 16-0CT-2001 (Rel. 40, Last annotation update) Tumor necrosis factor ligand superfamily member apoptosis inducing ligand) (TRAIL protein). TNFSF10 OR TRAIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00207; TNF; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Mammalia; Eutheria;
                                                                                                                                               "Identification and characterization family that induces apoptosis."; Immunity 3:67-682(195).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
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                                                SUBUNIT: HOMOTRIMER (POTENTIAL).
SUBCELLULAR LOCATION: Type II membrane protein (Potential).
TISSUE SPECIFICITY: WIDESPREAD.
SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PAASRSMFVALLGLGLGQVVCSVALFFYFRAQMD--PNRISEDGTHCIYRILRLHENADF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMVYVTKTSIKIPSSHTLMKGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 280
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SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
EXTRACELLULAR (POTENTIAL).
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Pred. No. 3.7e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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CARBOHYD
SEQUENCE
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PROSITE; PS50049; TNF_2; 1.

CYCOKINE; Transmembrane; Signal-anchor; Apoptosis.

CYCOKINE; Transmembrane; Signal-anchor; CPOTENTIA

DOMAIN

1 17

TRANSMEM 18 38

EXTRACELLULAR (POTENTIA

DOMAIN 39 291

EXTRACELLULAR (POTENTIA

CARBOHYD 52 52

CARBOHYD 53 52

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ProDom; PD008600; TNF_5; 1
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InterPro; IPR003636; TNF_ab
                                                                                                                                                                                                                                                                                   TASL_HUMAN STANDARD; PRT; 2
P48023;
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
FAS antigen ligand (Apoptosis antigen
TNFSF6 OR APTILG1 OR FASL.
   Alderson M.;
"Fas ligand
                                                              SEQUENCE FROM N.A. MEDLINE=95105731; PubMed=7528780;
                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                        Homo sapiens (Human)
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European Bioinformatics Institute There a
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Primates;
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Pred. No. 7.7e
52; Mismatches
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EXYTRACELLULAR (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
; 3FEACAB9F0D7D802 CRC64;
                                                                                                                                                                                                Craniata; Vo
Catarrhini;
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                                                                                                                                                                                                                                 Vertebrata;
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InterPro: IPR003263; TNF_5.
InterPro: IPR003636; TNF_abc.
InterPro: IPR00478; TNF_family.
Pfam; PF00229; TNF; 1.
ProDom; PD002012; TNF_abc; 1.
ProDom; PD00860; TNF_5; 1.
SMART; SM00207; TNF; 1.
                            Cytokine;
Antigen.
                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MATSUMURE M., NAKANISHI Y., Ohba Y.;
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.

-I- FUNCTION: CYTOKINE THAT BINDS TO FAS ANTIGEN, A RECEPTOR THAT TRANSDICES THE APOPTOTIC SIGNAL INTO CELLS. MAY BE INVOLVED IN CYTOTOXIC T CELL MEDIATED APOPTOSIS AND IN T CELL DEVELOPMENT.

FAS-ANTIGEN MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED SUICIDE OF MATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-95071350; Put
Mita E., Hayashi N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=95127560; PubMed=7826947;
Takahashi T., Tanaka M., Inazawa J.,
"Human Fas ligand: gene structure, ci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM Schaetzlein C
                                                       PROSITE; PS00251; TNF_1; PROSITE; PS50049; TNF_2;
                                                                                                                                                                                       MIM; 134638;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-10 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (MAY-1997) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochem. Blophys. Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fusamoto H., Kamada
"Role of Fas ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lymphocytes.";
J. Exp. Med. 181:71-77(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Int. Immunol. 6:1567-1574(1994).
                                                                                                                                                                                                                                                                                                                                                                                                     SURFACE.
SINILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
SINILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
DATABASE: NAME-PROW, NOTE-CD guide CD178 entry;
WWW-"http://www.ncbi.nlm.nih.gov/prow/guide/3338769674_g.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T CELLS, OR BOTH.
SUBUNIT: HOMOTRIMER (PROBABLE).
SUBCELLULAR LOCATION: TYPE II M
                                                                                                                                                                                                               X89102; CAA61474.1; -.

Y008137; AAC50071.1; -.

Y011821; AAC50124.1; -.

D38122; BAA07320.1; -.

Z96050; CAB09424.1; -.

AB013303; BAA32542.1; -.
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                                                                                                                                                                                                   P06804; 2TNF.
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                                         Transmembrane;
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995) to the
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N., Ilo S., Takehara
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102
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                                        Glycoprotein; Signal-anchor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FLUID,
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 CYTOPLASMIC (E
SIGNAL-ANCHOR
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BY CLEAVAGE FORM THE CEL
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MEMBRANE PROTEIN)
                                        Apoptosis;
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RESULT 6
FASL_MOUSE
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Best Local
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CARBOHYD
CARBOHYD
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SEQUENCE
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TNFSF6 OR APTILG1 OR FASL OR GLD.
  SEQUENCE FROM N.A. (ISOFORM FASL).
MEDLINE-95196085; PubMed-7889405;
Lynch D.H., Watson M.L., Alderson;
Tough T., Gibson M., Davis-Smith T
                                                                                                                                                                                                                                                                                      "Generalized lymphoproliferative disease mutation in the Fas ligand."; Cal 76:969-976(1994).
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM FASL).
MEDLINE-94185175; PubMed-7511063;
Takahashi T., Tanaka M., Brannan C
                                                                                                                                    Peitsch M.J., Tschopp J.J.;
"Comparative molecular modelling of the TNF family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                   MEDLINE-95388076; PubMed-7544870,
                                                                                                                                                                                                                            STRAIN-C57BL/6
                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                            Suda T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia; Eutheria; Rodentia; Sciurognathi; NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       211
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                                                                                                               Immunol.
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BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL);
A8A6EB358246E9BB CRC64;
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Pred. No. 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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T., Smith C
                                                                                                                                                           of
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                                                                                                                                                                                                                                                 AND
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                                                                                                                                                                                                                                               3D-STRUCTURE
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Pfam; PF00229; TNF; 1.
ProDom; PD002012; TNF_abc; 1.
ProDom; PD008600; TNF_5; 1.
SMART; SM00207; TNF; 1.
PROSITE; PS00251; TNF_1; 1.
PROSITE; PS00251; TNF_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHARACTERIZATION OF VARIANT GLD.

MEDLINE-96091792; Pubmed-7495745;

Hahne M., Peitsch M.C., Irmler M., Schroeter M., Lowin B.,

Rousseau M., Bron C., Renno T., French L., Tschopp J.;

"Characterization of the non-functional Fas ligand of gld mice.";

Int. Immunol. 7:1381-1386(1995).

Int. Immunol. 7:1381-1386(1995).

TRANSDUCES THE APOPTOTIC SIGNAL INTO CELLS. MAY BE INVOLVED IN

CYTOTOXIC T CELL MEDIATED APOPTOSIS AND IN T CELL DEVELOPMENT.

PERLPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED SUICIDE OF MATURE

T CELLS, OR BOTH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=C3H. TISSUE=Spleen;
MEDLINE=20021694; PubMed=10552956;
Ayroldi E., D'Adamio F., Zollo O., Agostini M., Moraca R.,
Cannarile L., Migliorati G., Delfino D.V., Riccardi C.;
"Cloning and expression of a short Fas ligand: A new alternatively
spliced product of the mouse Fas ligand gene.";
Blood 94:3456-3467(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunitý
[4]
Cytokine; Transmembrane; Glycoprotein; Signal-anchor; I Disease mutation; Alternative splicing.

DOMAIN 1 78 CYTOPLASMIC (POTENTIAL).

TRANSMEM 79 100 SIGNAL-ANCHOR (TYPE-II ME)

DOMAIN 101 279 EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                HSSP: P01375; 4TSV.
MGD; MGI:99255; Tnfsff.
InterPro; IPR003263; TNF_5.
InterPro; IPR003636; TNF_abc.
InterPro; IPR000478; TNF_family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          between the Swiss Institute of Bioinf
the European Bioinformatics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        two
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=BALB/C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Mus musculus Balb/c
two amino acids.";
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family gene cluster.";
unity 1:131-136(1994).
                                                                                                                                                                                                                                                                                           L; U06948; AAA17800.1; -.
L; U10984; AAA19778.1; -.
L; S76752; AAB33780.1; -.
L; U58999; AAB62915.1; -.
L; AF119335; AAD52106.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LYMPHOPROLIFERATION DISEASE (GLD), AN AUTOSOMAL RECESSIVE DI
RESPONSIBLE FOR LYMPHADENOPATHY AND AUTOANTIBODY PRODUCTION.
SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INTERACTION.
DISEASE: A D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T CELLS, OR BOTH.
SUBGULT: HOMOTRIMER (PROBABLE).
SUBCELLULAR LOCATION: ISOFORM FASL IS A TYPE II MEMBRANE PROTEIN.
ISOFORM FASLS IS SOLUBLE.
ALTERNATIVE PRODUCTS: 2 ISOFORMS; FASL (SHOWN HERE) AND FASLS; ARE
PRODUCED BY ALTERNATIVE SPLICING. ISOFORM FASL MEDIATES APOPTOSIS
WHILE ISOFORM FASLS PREVENTS APOPTOSIS INDUCED BY FAS/FASL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through a collaboration -
een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MAY-1996) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A DEFICIENCY IN THIS PROTEIN DISEASE (GLD), AN
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                        (TYPE-II MEMBRANE PROTEIN)
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                                                                         Apoptosi
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Best Local :
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P51749;
01-OCT-1996
01-OCT-1996
30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
CARBOHYD
CARBOHYD
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VARIANT
VARIANT
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DOMAIN
DISULFID
CARBOHYD
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GP39)
                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                           Mertens B.E.L.C., Muriuki M., Gaidulis L.; "Cloning of two members of the TNF-superfamily
                                                                                                                                                                                                  Bos taurus (Bovine)
Eukaryota; Metazoa;
                                                                                                                                                                                                                        TNFSF5 OR CD40LG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VARIANT
                                                                    and tumor necrosis factor alpha."; Immunogenetics 42:430-431(1995).
                                                                                                                MEDLINE=96006582;
                                                                                                                                rissue=Blood;
                                                                                                                                                                NCBI_TaxID=9913;
                                                                                                                                                                            Bovidae; Bovinae;
                                                                                                                                          SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                      232
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         FUNCTION: MEDIATES B-CELL PROLIFERATION IN THE ABSENCE OF STIMULUS AS WELL AS IGE PRODUCTION IN THE PRESENCE OF IL-4 INVOLVED IN IMMUNOGLOBULIN CLASS SWITCHING (BY SIMILARITY) SUBUNIT: HOMOTRIMER.
SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXIST
                                                                                                                                                                                                                                                                                                                                                                 NISQLSLINFEESKTFFGLYKL
                                                                                                                                                                                                                                                                                                                                                                                       EVSNPSLLDPDQDATYFGAFKV
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70; Conservative
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                                                                                                                                                                                                                                                         (Rel. 34,
(Rel. 34,
(Rel. 39,
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                                                                                                                                                                                                                                                (TNF-related activation
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                                                                                                                   PubMed=7590981;
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21.7%;
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N-LINKED (GLCNAC...) (POTEN
N-LINKED (GLCNAC...) (POTEN
N-LINKED (GLCNAC...) (POTEN
MISSING (IN ISOPORM FASLS).
T -> A (IN STRAIN BALB/C).
E -> G (IN STRAIN BALB/C).
F -> L (IN GLD; ABOLISHES BIN
TO ITS RECEPTOR).
                                                                                                                                                                                                                                                                                                                                                                                         313
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Pred. No. 1.8e-08;
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(BY
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 SIMILARITY)
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             EXISTS
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RESULT
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Best Local S
Matches 70
                SEQUENCE FROM N.A.
MEDLINE-94084792; PubMed-7505205;
Suda T. Takahashi T., Golstein P.,
"Molecular cloning and expression o
                                                                                                                                                                       TNFSF6 OŘ APTIĹGI OR FASL.
Rattus norvegicus (Rat).
Eukaryota, Metazoa; Chordata;
Mammaila; Eutheria; Rodentia;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
DISULFID
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                    01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last seq
15-JUL-1999 (Rel. 38, Last ann
EAS antigen ligand.
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InterPro; IPR000478; TNF_family.
Pfam; PF00229; TNF; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IVNQDGFYYLYANICFRHHETSGDLATEYLQLMVYVTKTSIKIP--SSHTLMKGGSTKYW
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PS00251: THE 1: 1.

PS00251: THE 1: 1.

PS50049: THE 2: 1.

CYTOPLASMIC (POTENTIAL).

SIGNAL-ANCHOR (TYPE-II MEMBRANE F. COTENTIAL).

OOTENTIAL).
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218
240
29242
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annotation update)
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EXTRACELLULAR (POTENTIAL).

POTENTIAL.

N-LINKED (GLCNAC. .) (POT
4M; 8491FEFB30A787FD CRC64;
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Pred. No. 7.9e-
54; Mismatches
                                                                                                                                                                                                       Craniata; Vertebrata;
Sciurognathi; Muridaé;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -ETLSOAPFIASLCLKSPSGSERILLRAANTH--
                of the Fas ligand, a novel
                                                    Nagata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          278
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nes 122;
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; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
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                      member
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Best Local S
Matches 64
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PROSITE; PS00251; TNE_1; 1.

PROSITE; PS00251; TNE_2; 1.

Cytokine; Transmembrane; Glycoprotein; Signal-anchor; Apoptosis.

Cytokine; Prositional Apoptosis.

Cytokine; Prositional Apoptosis.

Cytokine; Prositional Apoptosis.

Cytokine; Signal-anchor; Apoptosis.

Cytokine; Transmembrane; Glycoprotein; Signal-anchor; Apoptosis.

Transmembrane; Glycoprotein; Apoptosis.

Transmembrane; Glycoprotein; Apoptosis.

Transmembrane; Glycoprotein; Apoptosis.

Transmembrane; Glycoprotein; Apoptosis.

Transmembrane; Apoptosis.

Transmembrane; Glycoprotein; Apoptosis.

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CARBOHYD
SEQUENCE
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DOMAIN
DOMAIN
DISULFID
CARBOHYD
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      206 HKVYM--RNFKYPGDLVLMEEKKLNYCT-TGQIWAHSSYLGAVFNLTVADHLYVNISQLS
                                                                                                                                                                                                                                                                                                                                                                                        97
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                                                                 LMVYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPS
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                                                                                                                                                                GSHKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQ
                                                                                                                                                                                                                                                                                                                   RIKQAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPS
                                                                                                                                                                                                                                                                                                                                                                              G-----MYQLFHLQKELAELREFTNHSL-RVSSFEKQIANPSTPSETKKPRSV----
                                                                                                                                                                                                                                                                                                                                                                                                                                         GQVVCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCR 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GPGQRRPPP--PPPPPSPLPPPSQPPPLPPLSPLKKKDNIELWLPVIFFMVLVALVGMGL 96
                                                                                                                                   -SRSIPL-EWEDTYGTALISGVKYKKGGLVINEAGLYFVYSKVYFRGQSCN----
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100
45
199
116
247
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31140

MW;

POLY-PRO.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (PO'N-LINKED (GLCNAC. . .) (PO'N-LINKED (GLCNAC. . .) (PO'N-LINKED (GLCNAC. . .) (PO'N) 2898E18A862CEAC6 CRC64;

(POTENTIAL). (POTENTIAL)

(TYPE-II MEMBRANE PROTEIN).

10.4%;

47;

Pred. Score 175.5; Mismatches

No. 1e-07

106;

Indels Length

Gaps

10;

----FVALLGLGL

57

SQPLS

262 297 205 237 151 177 143

DB

278; 99;

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InterPro; IPRO03263; TNE_5.
InterPro; IPRO03636; TNE_abc.
InterPro; IPRO03636; TNE_family.
InterPro; IPRO0478; TNE_family.
Pfam; PF00229; TNF; 1.
ProDom; PD008600; TNF_abc; 1.
ProDom; PD008600; TNF_5; 1.
SMART; SM00207; TNF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cell 75:1169-1178(1993).

-I- FUNCTION: CYTOKINE THAT BINDS TO FAS ANTIGEN, A RECEPTOR THAT TRANSDUCES THE APOPTOTIC SIGNAL INTO CELLS. MAY BE INVOLVED IN CYTOTOXIC T CELL MEDIATED APOPTOSIS AND IN T CELL DEVELOPMENT.

FAS-ANTIGEN MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED SUICIDE OF MATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for content entities requires a license agreement (See http://www.isb-sib.ch/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.com/arcord.org.c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U03470; AAC52129.1; -. HSSP; P01375; 4TSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KIDNEY AND LUNG.
INDUCTION: BY PMA/IONOMYCIN AND CONCAVALIN/INTERLEUKIN-2.
SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE SPECIFICITY: EXPRESSED THYMOCYTES. MODERATE OR WEAK I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: TYPE II MEMBRANE INTO THE EXTRACELLULAR FLUID, PROBABLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T CELLS, OR BOTH.
SUBUNIT: HOMOTRIMER (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EXPRESSION FOUND
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BY CLEAVAGE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPLENOCYTES
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INTESTINES
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298 263

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AC CONTRACTOR OF THE CONTRACT 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
CD40 ligand (CD40-L) (TNF-related acti
antigen GP39) (CD154 antigen).
TNFSF5 OR CD40LG OR CD40L OR TRAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Aruffo A., Farrington M., Hollenbaugh D., Li X., Milatovich A., Nonoyama S., Bajorath J., Grosmaire L.S., Stenkamp R., Neubauer Roberts R.L., Noelle R.J., Ledbetter J.A., Francke U., Ochs H.D. "The CD40 ligand, gp39, is defective in activated T cells from patients with X-linked hyper-IgM syndrome."; Cell 72:291-300(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=93049181; PubMed=1385114;
Hollenbaugh D., Grosmaire L.S., Kullas
Braesch-Andersen S., Noelle R.J., Stame
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND VARIANTS HIGHI 128-ARG-GLY-129 MEDLINE=93145330; Pubmed=7678782;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eur. J.
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                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE-93138085;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Spriggs M.K., Armitage R.J., Strockbine L., Macduff B.M., Sato T.A., Maliszewski C.R., "Recombinant human CD40 ligand stimulates B immunoglobulin E secretion.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The
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                  "2-A crystal
ligand.";
                                                                                                                                                                                                     Shimadzu
                                                                                                                                                                                                                                                                                                                                           Gauchat J.F.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE=93094757; PubMed=1281209;
                                                                           Karpsusas
                                                                                                    MEDLINE=96131874;
                                                                                                                     X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS)
                                                                                                                                                               Submitted
                                                                                                                                                                                                                                                                                regulation
                                                                                                                                                                                                                                                                                                       "Human
                                                                                                                                                                                                                                                                                                                            Bonnetoy
                                                                                                                                                                                                                                                                                                                                                                                                                           immunoglobulin E secretion.";
J. Exp. Med. 176:1543-1550(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human T cell antigen gp39, a member nd for the CD40 receptor: expression B cell co-stimulatory activity.";
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                                                                                                                                                                                                                                                                                                       CD40-ligand:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     =93076854; PubMed=1280226;
, Korthaeuer U., Mages H.W.,
g of TRAP, a ligand for CD40
Immunol. 22:3191-3194(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11:4313-4321(1992).
                                                                                                                                                                                                   .
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                                                                                                                                                                                                                        FROM
                                                          Thomas D.
                                                                                                                                                               (FEB-1995)
                                                                                                                                                                                                                                                               O-ligand: molecular of expression by fa 315:259-266(1993).
                                                                                                                                                                                                     Terasaki H.,
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                                                                                                                                                                                                                                                                                                                                           5; PubMed=7678552;
Aubry J., Mazzei
                                                                               Y.-M., Wang
                                                                                                    PubMed=8589998;
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                                         of an
                                                                                                                                                               the
                                                                                                                                                                                                     Ninomiya
                                                                                                                                                               EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                    factors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata;
Catarrhini; Hominidae
                                            extracellular
                                                                                                                                                                                                                                                                                    cloning, cellular actors controlling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                 J.-H.,
                                                                                                                                                                                                                                                                                                                                               G
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                                                                                                                                                                                                                                                                                                                                             .J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Senger G.
                                                                                                                                                                                                     R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  261
                                                                                 Thompson
                                                                                                                       OF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C
                                                                                                                                                                                                                                                                                                                                               Life
                                                                                                                                                                                                       Shimizu
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, Fanslow W.
B cell prol
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                                            fragment of
                                                                                                                                                                                                                                                                                                                                               ₽.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the TNF gene family, a soluble form of gp
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                                                                                 J.,
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MEDLINE=93156839; PubMed=7679206;
Korthaeuer U., Graf D., Mages H.W.,
Malcolm S., Ugazio A.G., Notarangelo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Defective expression of T-cell immunodeficiency with hyper-IgM. Nature 361:539-541(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=98266353;
Singh J., Garber I
Zheng Z., Naismit
                                                                                                                                                                                                                                                                                                                                         Lin Q., Rohrer J., Allen R.C., Larche I Gatti R.A., Derauf D.C., Belmont J.W.,
                                                                                                                                                                                                                                                                                                                                                                   VARIANTS HIGM1 PRO-155 AND VAL-227, AND MEDLINE-96133533; PubMed-8550833;
                                                                                                                                                                                                                                                                                                                                                                                                         Cavagni G., Reznick I., Levy J., Zan-Bar I Plebani A., Vezzoni P., Notarangelo L.D.; Plebani A., Vezzoni p., Notarangelo L.D.; "Characterization of nine novel mutations patients with X-linked hyper IgM syndrome hm. J. Hum. Genet. 56:898-906(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARÍANTS HIGM1 ALA-126; ARG-140 AND GLU-144.

MEDLING=9523438; PubMed=7717401;

Macchi P. Villa A., Strina D., Sacco M.G.,

Giliani S., Mantuano E., Fasth A., Andersson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "CD40 ligand mutations in Nature 361:541-543(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disanto J.P., Bonne
de Saint Basile G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-93156840; PubMed=8094231; Disanto J.P., Bonnefoy J.Y., Gauchat
                                                                                                                                                                                        Yata J.-I., Och H.D.;
"Mutations of the CD40 ligand gene
"Mutations of the XVndrome.";
                                                                                                                                                                                                                                                                                                    Efficient mutation analysis
IgM syndrome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Science 259:990-993(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "CD40 ligand
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                                                                                                                                                                                                                                Nonoyama S.,
                                                                                                                                                                                                                                              MEDLINE=97295077; PubMed=9150729;
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                                                                                                                                                                                                                                                                                                  IgM
                                                                                           SUBUNIT: HOMOTRIMER.
SUBUNIT: HOMOTRIMER.
SUBCELLULAR LOCATION: TYPE
SUBCELLULAR SOLUBLE FORM.
DISEASE: DEFECTS IN THESES ARE THE CAUSE OF AN X-LINKED IMMUNODEFICIENCY WITH HYPER-IGM (HIGMI), AN IMMUNOGLOBU SWITCH DEFECT CHARACTERIZED BY ELEVATED CONCENVRRATIONS IGM AND DECREASED AMOUNTS OF ALL OTHER ISOTYPES. AFFECT PRESENT AT AN EARLY AGE (USUALLY WITHIN THE FIRST YEAR
                                                                                                                                   FUNCTION: MEDIATES B-CELL PROLIFERATION IN THE ABSENCE STIMULUS AS WELL AS IGE PRODUCTION IN THE PRESENCE OF INVOLVED IN IMMUNOGLOBULIN CLASS SWITCHING.
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g Z., Naismith J.H., Thomas D.,
role of polar interactions in
its receptor CD40.",
ein Sci. 7:1124-1135(1998).
                                                                   T-LYMPHOCYTES
                                                                                TISSUE SPECIFICITY:
                                                                                                                                                                             Genet.
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et. 99:624-627(1997)
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to L.D.,
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  OTHER ISOTYPES. AFFECTED MALES WITHIN THE FIRST YEAR OF LIFE)
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for X-linked l
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Of
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on B., Zegers
., Porat Y., A
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rinsky R.J.,
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IMMUNOGLOBULIN ISOTYPE
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Matches
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Best Local
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EMBL; Z15017; CAA78737.1; -.
EMBL; Z35018; CAA48077.1; -.
EMBL; L07414; AAA35662.1; -.
EMBL; D31797; BAA06599.1; -.
EMBL; D31793; BAA06599.1; JOINED.
EMBL; D31794; BAA06599.1; JOINED.
EMBL; D31795; BAA06599.1; JOINED.
EMBL; D31795; BAA06599.1; JOINED.
EMBL; D31795; BAA06599.1; JOINED.
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                                                                                                                                                          VARIANT
                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00251; TNF_1; 1.
PROSITE; PS50049; TNF_2; 1.
Cytokine; Transmembrane; Glycoprotein; Signal-anchor;
                                                                                                                                                                                                           VARIANT
                                                                                                                                                                                                                                                                                                   DOMAIN
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InterPro; IPR000478; TNF_fe
Pfam; PF00229; TNF; 1.
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                                                                                                                                                                                  VARIANT
                                                                                                                                                                                                                                    VARIANT
                                                                                                                                                                                                                                                                                                                                         Antigen; Disease mutation; DOMAIN 1 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                     103 -TLESQDTKLIPDSCRRIKQAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLE 161
70 QRCNTGERSLSLLNCEEIKSQFEGFV-KDIM-----
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                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RECURRENT BACTERIAL AND OPPORTUNISTIC INFECTIONS, INCLUDING PNEUMOCYSTIS CARINII PNEUMONIA AND INTRACTABLE DIARRHEA DUE TO CREPTOSPORIDIUM INFECTION. DESPITE SUBSTITUTION TREATMENT WITH INTRAVENOUS IMMUNOGLOBULIN, THE OVERALL PROGNOSIS IS RATHER POO WITH A DEATH RATE OF ABOUT 10% BEFORE ADDIESCENCE.

SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.

DATABASE: NAME-CD40Lbase;

DATABASE: NAME-CD40Lbase;

ETP-"ftp://www.expasy.org/cd40lbase/";

FTP-"ftp://www.expasy.org/cd40lbase/";

DATABASE: NAME-PROW; NOTE-CD guide CD154 entry;
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S28852;
JH0793;
                                                                        SRSMFVALLGLGL-GQVVCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDT-
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S26694;
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SM00207; TNF; 1.
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                                                                                               Score 158.5; DB 1;
Pred. No. 2.7e-06;
"Mamatches 113;
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Query Match Best Local S Matches 68

Similarity

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Conservative

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                                                                                                           PROSITE; PS00251; TNF_1; 1
PROSITE; PS50049; TNF_2; 1
Cytokine; Transmembrane; G
DOMAIN 1 22
TRANSMEM 23 46
  DISULFID
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
CD40 ligand (CD154 antigen).
TNFSF5 OR CD40LG OR CD40L.
                                                                                                                                                                                                                            ProDom; PD00860
SMART; SM00207;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long modified and this statement is not removed.
                                                                   DOMAIN
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InterPro; IPR000478; TNF_family.
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TNF5_FELCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hosie M.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Thymus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Felis silvestris catus (Cat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SWISS-PROT entry is copyright. It is produced through a ceen the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LGGVFELQPGASVFVNVTDPSQVSHGTGFTSFGLLKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VGGFFKLRSGEEISIEVSNPSLLDPDQDATYFGAFKV 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QVTFCSNREASSQAP-----FIASLCLKSPGRFERILLRAANTH--SSAKPCGQQSIH 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NICFRHHETSGDLATEYLQLMYYVTKTSIKIPS--SHTLMKGGSTKYWSGNSEFHFYSIN 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PQIAAHVISEAS-----SKTTSVLQW-AEKGYYTMSNNLVTLENGKQLTVKRQGLYYIYA 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AQPFAHLTINATDIPSGSHKVSLSSWYHDRGWAKISN--MTFSNGK-LIVNQDGFYYLYA
                                                                                                                                                                                                                            PD008600; TNF_5; 1.
SM00207; TNF; 1.
47
177
239
260
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                                                                                                                                                                                                                                                                        TNF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
  260
217
239
28727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chordata; (Carnivora;
                                                                                                                                                     Glycoprotein;
    WW.
                     N-LINKED (GLCNAC
                                                                                                  COPTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                          EXTRACELLULAR (POTENTIAL).
POTENTIAL.
                                                                                        (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Fissipedia; Felidae; Felis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
349FA0391FB7B932 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        as its content
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                  (POTENTIAL)
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L outstation -
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RESULT 11
TNFA_CAVPO
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01-OCT-1996
                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-1996 (Rel. 30-MAY-2000 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                factor-alpha.";
Am. J. Physiol. 273:L524-L530(1997).
Am. J. Physiol. 273:L524-L530(1997).
-i- FUNCTION: THE IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKIN WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF CERTAIN TUMOR CELL LINES, IT IS INFLICATED IN THE INDUCTION OF CACHEXIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION OR BY STIMULATION OF INTERLECKIN 1 SECRETION, IT CAN STIMULATE CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (NOV-1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-HARTLEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertek
Mammalia; Eutheria; Rodentia; Hystricognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TNF OR TNFA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tumor
               EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97462215; PubMed=9316485;
White A.M., Yoshimura T., Smith A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-DUNKIN-HARTLEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yuan
                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFA_CAVPO
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                                                     send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                   SUBUNIT: HOMOTRIMER (BY SIMILARITY).

SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXTRACELLULAR SOLUBLE FORM (BY SIMILARITY).

PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM PROTEDLYTIC PROCESSING (BY SIMILARITY).

DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES.

CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL
                                                                                                                                                                                                 SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY
                                                                                                                                                                                                                  CANCER AND INFECTION, AND MALNUTRITION.
                                                                                                                                                                                                                                                                                                                                                                  CONDITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSWLDLAKRSKLEAQPFAHLTINATDIPSGSHKVSLSSWYHDRGWAKISN--MTFSNGK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LRLHENADFQDTTLESQ--DTKLIPDSCRRIKQAFQGAVQKELQHIVGSQHIRAEKAMVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLDPDQDATYFGAFKV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LIVNQDGFYYLYANICFRHHETSGDLATEYLQLMYYVTKTSIKIP--SSHTLMKGGSTKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RNLYEDFVFMKTLQKCNKGEGALSLLNCEEIKSRFEAF----LKEIMLNKETKKEKNVA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APRSVAP--GPPVSMKIFMYLLTVFLITQMIGSALFAVYLHRRLD--KIEDE------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----MQKGDQDPRVAAHVISEAS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Y-2000 (Rel. 39, Last annotation update) necrosis factor precursor (TNF-alpha) (Cachectin)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -SSSKPCGQQSIHLGGVFELHPGASVFVNVTDPSQVSHGTGFTSFGLLKL
U39839;
U77036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T., Kelly F.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                inflammation induced by recombinant
AAB06492.1;
AAB19210.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Lung,
y F.J., Bing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . 34, Created)
. 34, Last sequence . 39, Last annotation.
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Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Smith A.W., Westwick J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            le C.D.;
EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -SSTASVLQW-APKGYYTISSNLVTLENGKQ
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                                                                                                                                                                                                                                       DISEASES, INCLUDING BY GENERAL ILL HEAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Watson M.L.;
pig tumor necrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <u>..</u>
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TNF5_CANFA
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                     097626;
16-OCT-2001
16-OCT-2001
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DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00251; TNF_1; 1.
PROSITE; PS50049; TNF_2; 1.
PROSITE; PS50049; Transmembrane;
nv SIM
                                                                                                                      Hosie M.H., Willett B.J.;

"Adjuvant properties of canine CD40L.";

"Adjuvant properties of canine CD40L.";

"Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.

"SUBMITTION: MEDIATES B-CELL PROLIFERATION IN THE ABSENCE OF IL-4

INVOLVED IN IMMUNOGLOBULIN CLASS SWITCHING (BY SIMILARITY).

"I-SUBUNIT: HOMOTRIMER (BY SIMILARITY).

"SUBCELLULAR LOCATION: TYPE II MEMBRAME PROTEIN. ALSO EXIST

EXTRACELLULAR SOLUBLE FORM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                             TNFSF5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ProDom; PD002012; TNF_abc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR01234; TNECROSISFCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00229; TNF; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P06804; 2TNF.
InterPro; IPR003636;
InterPro; IPR000478;
                     use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                 This
                                                                                                                                                                                                                                                                                                                   Canis familiaris
                                                                                                                                                                                                                                                                                                                                                                                                        TNF5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROPEP
                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                           NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
                                                                        the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                          Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          134 IVGSQHIRAEKAMVDGSWLDLAKRSKLEA-----QPFAHLTINATDIPSGSHKVSLSS 186
                                                                                     between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NLPQYLDFADSGQIYFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WYHDRGWAKISN-MTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMVYVTKT
                                                                                 SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AVSYPEKVNLLSAIKSPCQKETPEGAERKPW-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WLSKRANALLANGMGLSDNQLVVPSDGLYLIYSQVLFK-----GQGCPSYLLLTHTVSRL
                                                                                                                                                                                                                                                                                                                                                                                                       CANFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SNPSLLD-PDQDATYFG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50;
                                                                                                                                                                                                                                                                                                                             OR CD40LG OR CD40L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                        Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Carnivora; Fissipedia; Canidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80
36
147
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(Rel. 40, Last seq
(Rel. 40, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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234
56
178
25793 .
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                                                                                                                                                                                                                                                                                                                   (Dog).
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Pred. No. 2.7e-05;
"''matches 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mbrane; Glycoprotein; Signal-anchor.
BY SIMILARITY.
TUMOR NECROSIS FACTOR.
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
BY SIMILARITY.
; 7272C940393E7E9B CRC64;
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                                      http://www.isb-sib.ch/announce/
                                                Usage
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01-JAN-1988 (Rel. 0
01-MAR-1989 (Rel. 1
30-MAY-2000 (Rel. 3
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DISULFID
CARBOHYD
                                                                                                                         SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-88224564; Pubmed-2836146;
Shirai T., Shimizu N., Shiojiri S., Horiguchi S.
Shirai T., Shimizu N., Shiojiri S., Horiguchi S.
                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; NCBI_TaxID=10090;
                                                      MEDLINE-85298296; Pul
Pennica D., Hayflick
Goeddel D.V.;
                                                                                                                                                                                                                                    Tumor necrosis factor TNF OR TNFA.
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SEQUENCE
                   "Cloning and expression
tumor necrosis factor.";
Proc. Natl. Acad. Sci. (
                                                                                       SEQUENCE FROM N.A.
                                                                                                                       "Cloning and expression tumor necrosis factor.";
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PS50049; TNF_2; 1.
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39,
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ick J.S., Bringman
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Last annotation update)
precursor (TNF-alpha) (
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CYTOPLASMIC (POTENTIAL):
SIGNAL-ANCHOR (TYPE-II MEMBRANE P)
(POTENTIAL).
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
N-LINKED (GLCNAC...) (POTENTIAL)
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Pred. No. 3.7e-05;
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                       82:6060-6064(1985)
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X-RAY CRYSTALLOGRAPHY (1.4 ANGSTROMS) OF 80-235.

MEDLINE-99190964; PubMed-10089307;
Baeyens K.J., De Bondt H.L., Raeymaekers A., Fiers W., De Ranter The Structure of mouse tumour-necrosis factor at 1.4 A resolution towards modulation of its selectivity and trimerization.";
Acta Crystallogr. D 55:772-78(1999)
-I- FUNCTION: TWF IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTY WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION CACHEXIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACT
                                                                                                                                                                                                                                      "Alternative cleavage of the cachectin/tumor necrosis factor propeptide results in a larger, inactive form of secreted pr \sigma. Biol. Chem. 264:16256-16260(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=87298639; Shakhov
                                                                                                                                                                           Kriegler M., Perez X., Defay K., Albert ?
"A novel form of TNF/cachectin is a cell
                                                                                                                                                                                                     IDENTIFICATION OF MEMBRANE-BOUND MEDLINE=88165056; PubMed=3349526;
                                                                                                                                                                                                                                                                                          SEQUENCE OF 70-87. MEDLINE-89380231;
                                                                                                                                                                                                                                                                                                                              murine tumor necrosis factor.";
Biochem. Biophys. Res. Commun.
                                                                                                                                                                                                                                                                                                                                                   MEDLINE=91097531; PubMed=2268312; Sherry B., Juc D.-M., Zentella A., C"Characterization of high molecular
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 80-99. MEDLINE=91097531;
                                                                                                                                                                                                                                                                                                                                                                                                                 Ikegami H., Makino S., Yamato E., Kawaguchi Y., Ue
Takekawa K., Ogihara T.;
"Identification of a new susceptibility locus for
diabetes mellitus by ancestral haplotype congenic
J. Clin. Invest. 96:1936-1942(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-96013654;
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MEDLINE-88067722;
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Complete nucleotide
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Nucleic Acids Res. 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ruysschaert M.-R., Fiers W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fransen L., Mueller R., M
Kawashima E., Chollet A.,
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MEDLINE-85242112;
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                                                                                                                                                               transmembrane protein:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Semon D., Kawashima E., Jongeneel C.V., Shakhov A.N., Ne "Nucleotide sequence of the murine TNF locus, including (tumor necrosis factor) and TNF-beta (lymphotoxin) genes Nucleic Acids Res. 15:9083-9084(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caput D.,
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                                                                                                                                        53:45-53(1988).
                                                                                                                                                                                                                                                                                                                             Biophys.
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o S., Yamato E.,
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MGD; MGI:104798; Tnf.
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InterPro; IPR000478; TNF_family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This
                                                                                                                                                                                                                                 PROSITE; PS00251; TNF_1; 1. PROSITE; PS50049; TNF_2; 1.
                                                                                                                                                                                                                                                                                   Pfam; PF00229; TNF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities
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                                                                                                                                                                                          CHAIN
                                                                                                                                                                                                    PROPEP
                                                                                                                                                                                                                      Cytokine;
                                                                                                                                                                                                                                                       SMART;
                                                                                                                                                                                                                                                                 ProDom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
142
                                                             163
                    221 CFRHHETSGDLATEYLQLMVYVTK-----TSIKIPSSHTLMKGGSTKYWSGNS
                                         90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OR BY STIMUCELL PROLIFCONDITIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBUNIT: HOMOTRIMER. SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                     A27303;
A34251;
S03791;
                                                                                                                                                                                                                                                                                                                                                                                      D84194;
D84194;
D84195;
D84199;
D84197;
D84197;
D84198;
D84198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISEASE: CACHEXIA ACCOMPANIES CANCER AND INFECTION, AND IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EXTRACELLULAR SOLUBLE FORM.
PTM: THE SOLUBLE FORM DERIVES
                                                                                                                                                                                                                                                                                                                                                                     A22908;
A25164;
                                                                                                                                                                                                                                                                                                                                                                                                                      X02611; CAA26457.1;

X02055; AAA40462.1; A

X088296; AAA40459.1;

D84196; BAA19512.1;

D84194; BAA19512.1;

D84199; BAA19512.1;

D84199; BAA19513.1;

D84199; BAA19513.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROTEOLYTIC PROCESSING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; U06950; AAA18594.1;
; M13049; AAA40457.1;
; M11731; AAA40458.1;
; Y00467; CAA68530.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                             QPFAHLTINATDIPSGSHKVSLS-SWYHDRGWAKISN-MTFSNGKLIVNQDGFYYLYANI 220
                                         KPVAHVVAN----
                                                                                  l Similarity
42; Conser
                                                                                                                                                                                                                                                       SM00207;
                                                                                                                                                                                                                                                              PR01234; TNECROSISFCT PD002012; TNF_abc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MALNUTRITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              requires a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN
                                                                                                                                                                                                                       Cytotoxin; Transmembrane; Glycoprotein; Signal-anchor;
                                                                                                                                   231
235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                      A34251.
S03791.
                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                           A22908.
A25164.
A27303.
-GQGCPDYVLLTHTVSRFAISYQEKVNLLSAVKSPCPKDTPEGAELKPW----
                                                                                                                                                                                                                                                                                                                                                                                                    BAA19513.
BAA19513.
                                                                                                                                      ΑĄ;
                                                                                                                              79
235
56
179
86
86
231
25895 1
                                                                                                                                                                                                                                                       TNF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             license agreement (See http://www.isb-sib.ch/announce/
                                                                                           25 8
                                         HQVEEQLEWLSQRANALLANGMDLKDNQLVVPADGLYLVYSQV
                                                                                           . 48;
                                                                                                                                      MW;
                                                                                                                                                                                                                                                                                                                                                                                                              JOINED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE II MEMBRANE PROTEIN. FORM.
                                                                                  28;
                                                                               Pred. No. 6.50
8; Mismatches
                                                                                                                                             N-LINKED (GLCNAC.
G -> R (IN REF. 3
                                                                                           Score 141.5;
Pred. No. 6.
                                                                                                                                                                             TUMOR NECROSIS
SIGNAL-ANCHOR
                                                                                                                                    -> R (IN REF. 3 1 16DD2A9676D68C5D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S A VARIETY OF
CHARACTERIZED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FROM THE MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 There are no restrictions ng as its content is in
                                                                                             .5e-05;
                                                                                                                                                                              (TYPE-II
                                                                                                      DB 1;
                                                                                                                                                                                        FACTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Usage
                                                                                  57;
                                                                                                                                               AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISEASES, :
                                                                                                                                    AND 4).
CRC64;
                                                                                                     Length
                                                                                  Indels
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                                                                                                                                                                              MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and
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                                                                                  Gaps
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                    268
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                            Ito H.,
Hayashi
                                                                                                                                                                                                                                                                                                                                                                                                                                                [3]
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gene
[2]
EMBL; M12845; AAA31486.1; -. EMBL; M12846; AAA31482.1; -. EMBL; M60340; AAA31484.1; -. PIR; A25451; A25451.
PIR; A25454; A25454.
                                                                                    entities
                                                                                                   modified
                                                                                                                          the
                                                                                                                                                  This
                                                                                                                                                                                                                                                                                                                                                           "Molecular cloning and expression in Escherichia coli
coding for rabbit tumor necrosis factor.";
DNA 5:149-156(1986).
-I- FUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Structural analysis encoding TNF-beta (ly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryctolagus cuniculus (Rabbit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P04924;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RABIT
                                                                          or send an
                                                                                                                                     between
                                                                                                                                                                                                                                     ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nedospasov S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shakhov A.N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TNF OR TNFA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-AUG-1987 (Rel. 05,
13-AUG-1987 (Rel. 05,
15-JUL-1999 (Rel. 38,
Tumor necrosis factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TNFA_RABIT
                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=86219711; PubMed=3519137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=8621971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     factor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE~91065534;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Molecular cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         193
                                                                                                                                                                                                                                              SUBUNIT: HOMOTRIMER.
SUBCELLULAR LOCATION: TYPE
EXTRACELLULAR SOLUBLE FORM.
                                                                                                                                                                                                                                                                                                     FUNCTION: THE IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKINE MITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF CACHEXIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION OR BY STIMULATION OF INTERLEUKIN I SECRETION, IT CAN STIMULATE CELL PROLITERRATION AND THYPETCH OF THE PROLITERRATION OF INTERCLEUKIN I SECRETION.
                                                                                                                         European
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5:157-165(1986).
                                                                                                                                                                           SIMILARITY: BELONGS TO
                                                                                                                                                                                                                                                                                      CONDITIONS
                                                                                                                                                                                      AND
                                                                                                                                                                                                 CANCER AND INFECTION,
                                                                                                                                                                                                               DISEASE:
                                                                                                                                                                                                                         PTM: THE SOLUBLE FORM DERIVES PROTEOLYTIC PROCESSING.
                                                                                                                                    SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95:215-221(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---YEPIYLGGVFQLEKGDQLSAEVNLPKYLDFAESGQVYFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EFHFYSINVGGFFKLRSGEEISIEVSNPSLLD-PDQDATYFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          s=86219712; PubMed=3519138;
Shirai T., Yamamoto S., Ai
R.B.;
                                                                                                                                                                                                                                                                                                                                                                                                           Yamamoto S., Kuroda
H., Kato M., Seko M
                                                                                                                                                                                      MALNUTRITION
                                                                                      requires
                                                                                                   and this
                                                                                                             non-profit
                                                                                                                                                                                                                                                                                                 PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                 FROM
                                                                         nd this statement is not removed. equires a license agreement (See email to license@isb-sib.ch).
                                                                                                                         Bioinformatics Institute.
                                                                                                                                                                                                  CACHEXIA ACCOMPANIES

ND INFECTION, AND IS (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kuprash D.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (lymphotoxin) and TNF-alpha (tumor necrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=2249779;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lagomorpha;
                                                                                                             institutions as long
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                                                                                                                                                                                                                                                                                                                                                                                                            Seko M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene encoding
                                                                                                                                                                           THE TUMOR NECROSIS FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                      s.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rabbit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Azizov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                             II MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                         Sakamoto H., Kajihara J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Akira
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Leporidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cation update)
(TNF-alpha) (Cachectin)
                                                                                                                                                                                                  S A VARIETY OF
CHARACTERIZED
                                                                                                                                                                                                                                       FROM THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TNF locus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   M.M., Jongeneel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          update)
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X
                                                                                                                          There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rabbit tumor necrosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kawahara
                                                                                                              as its content
                                                                                      http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                              PROTEIN.
                                                                                                                                                                                                                                      MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryctolagus
                                                                                                 Usage
                                                                                                                                                                                                  DISEASES,
BY GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           231
                                                                                                                                                                                                                                                                                                                                                                                                  coli of
                                                                                                                                                                                                   GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C.V.
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                                                                                                                                                                                                                                                                ALSO
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RESULT TO PACE OF THE PACE OF 
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Best Local S
Matches 66
                                                                                                                                                                                                                                                                                                                         P23383;

01-NOV-1991 (Rel. 20, C

01-FEB-1994 (Rel. 28, I

15-JUL-1999 (Rel. 38, I

Tumor necrosis factor [
                                            TISSUE-Alveolar macrophage;
MEDLINE-92112044; pubMed-17
                                          SEQUENCE FROM N.A.
                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalla; Eutheria; Cetartiodactyla; Ruminantia; Pec
Bovidae; Caprinae; Ovis.
NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                          Ovis aries (Sheep).
                                                                                                                                                                                                                                                                                                               THE OR THEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SHEEP
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DISULFID
CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR01234; TNECROSISFCT.
ProDom; PD002012; TNF_abc; 1.
SMART; SM00207; TNF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cytokine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR003636; TNF_abc.
InterPro; IPR000478; TNF_family.
Pfam; PF00229; TNF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          197
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HSSP; P06804; 2TNF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LSAIKSPCHRETPEEAEPMAW-----YEPIYLGGVFQLEKGDRLSTEVNQPEYLDLAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SGOVYFG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANGMKLTDNOLVVPADGLYLIYSQVLF----SGQGCRSYVLLTHTVSRPAVSYPNKVNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SN-MTFSNGKLIVNODGFYYLYANICFRHHETSGDLATEYLOLMYYVTKTSIKIPSSHTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIKQAFQGAVQKELQHIVG
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56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PS00251; TNF_1; 1.
PS50049; TNF_2; 1.
; Cytotoxin; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    148
53
235
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                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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  PubMed=1765267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79
235
56
179
63
25816
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                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
precursor (TNF-alpha) (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8.3%;
                                                                                                                                                                                                                                                                                                                                                                                      Created)
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Pred. No. 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TUMOR NECROSIS FACTOR.
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
BY SIMILARITY.
MISSING (IN REF. 3).
; 610177D0BD2EF871 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -KPLAHVVAN----PQVEGQL----QWLSQRANALL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glycoprotein;
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nes 92;
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                                                                                             factor
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                                                                                                                                                                                                                                                                                                                         (Cachectin).
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                                                                                                                                                                                                                                            Pecora;
                                                                                         alpha cDNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                  Euteleostomi;
                                                                                                                                                                                                                                                Bovoidea;
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Query Match
Best Local S
Matches 52
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EMBL; X55152; CAA38952.1; -.
EMBL; X55756; CAA40076.1; -.
EMBL; A19163; CAA61445.1; -.
PIR; S13114; S13114
PIR; S20661; S20661.
PIR; JH0529; JH0529.
HSSP; P01375; 4TSV.
                                                                                                                                                                                     CHAIN
TRANSMEM
DISULFID
CARBOHYD
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                      PROSITE; PS00251; TNF_1; 1.
PROSITE; PS50049; TNF_2; 1.
Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Signal-anchor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the
                                                                                                                                                                                                                                                                                                                                   PRINTS; PR01234; TNECROSISFCT. ProDom; PD002012; TNF_abc; 1.
                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR003636; TNF_abc.
InterPro; IPR000478; TNF_family.
Pfam; PF00229; TNF; 1.
                                                                                                                                                                                                                                                                                                                          SMART; SM00207; TNF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
          101
                                    188
                                                                                        134
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"Sequence of the cDNA encoding owine tumor necrosis factor-alpha: problems with cloning by inverse PCR.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE-92155784; Pubmed-1786996;
                                                              55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'Molecular cloning, expression and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Andrews A.E., Nash A.D., Barcham
GQLRWGDSYANALMANGVELKDNQLVVPTDGLYLIYSQVLFRGHGCPSTPLFLTHTISRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT: HOMOTRIMER.
SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXTRACELLULAR SOLUBLE FORM.
PTW: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM PROTEOLYTIC PROCESSING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 veen the Swiss Institute of Bioinforma
European Bioinformatics Institute. The
by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UNDI. Cell Biol. 69:273-283(1991).

FUNCTION: THE IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKINE WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF CACHEXIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN
                        YHDRGWAKISNMTFSNG-----KLIVNQDGFYYLYANICFRHH-----ETSGDL
                                                                        IVGSQHIRAEKAMVDGSW---LDLAKRSKLEA---OPFAHLTINATDIPSGSHKVSLSSW 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF CANCER AND INFECTION, AND IS CHARACTERIZED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONDITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AND MALNUTRITION
                                                                                                                                Similarity
                                                                                                                                                                                                   78
36
146
96
                                                        -REEQSPAGPSFNRPLVQTLRSSSQASNNKPVAHVVAN---
                                                                                                                 Conservative
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56
178
96
63
25536 1
                                                                                                                              8.1%;
26.1%;
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                                                                                                                30;
                                                                                                           Score 137; DB 1; |
Pred. No. 0.00016;
); Mismatches 71;
                                                                                                                                                                                        SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
MISSING (IN REF. 1).
                                                                                                                                                                                                                                                   TUMOR NECROSIS FACTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of Bioinformatics and the I
Institute. There are no rest
tions as long as its content
                                                                                                                                                                                4BCF8CCAB7956B88 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G
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                                                                                                                                     Length 234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISEASES, INCLUDING BY GENERAL ILL HEAL
                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20
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                                                     --ISAP 100
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                                                                                                          Gaps
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В

043647 homo saplen
0961d2 homo saplen
097543 actus nancy
09myz2 capra hircu
09uiv3 homo saplen
070332 mesocricetu
09erg6 peromyscus
09ttj3 equus cabal
09bct5 tenrec ecau
09j127 rattus norv
09j126 rattus norv
09j126 rattus norv
09j127 actus norv
09j128 actus vocif
09ttg8 actus vocif
09ttg8 actus ratio
09bc538 actus vocif
09ttg8 actus ratio
09bc91 bradypus tr
09bc91 bradypus tr

O9bdm7 macaca neme
O99nd1 tamiascluru
O91z14 sigmodon hi
O28320 capra hircu
O9jm10 marmota mon

Q9bdc7 macaca mula
Q9i8d8 gallus gall
Q9qyh9 mus musculu
Q9qyh9 homo sapien 035853 mus musculu

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Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Maximum
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                             protein -
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                       1409
1396.5
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119
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                                                                                                                                                                                                                                                                                                                                                                                                                   No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein search, using sw model
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1: sp_archea:*

2: sp_bacteria

3: sp_fungi:*

4: sp_human:*

5: sp_invertebic:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organel1:

9: sp_plant:*

10: sp_plant:*

11: sp_rodent:

12: sp_virus:*

13: sp_vertebr:

14: sp_unclass:

15: sp_rvirus:*

16: sp_bacteri::

17: sp_archeap
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length: 2000000000
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Match
                       84. 4
82. 6
82. 6
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83. 9
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9. 9. 9
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Gapop 10.0 ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        July 8, 2002, 19:52:38; Search time 119.9 Seconds (without alignments) 457.376 Million cell updates/sec
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sp_organelle:*
sp_phage:*
sp_plant:*
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sp_fungi:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sp_mammal:*
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sp_archeap:*
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sp_rvirus:*
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sp_vertebrate:*
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287
199
53
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214
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282
282
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286
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1 Q9R1Y0
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1 Q9JJK9
1 Q9JJK8
1 Q9JJK8
1 Q9LZI9
3 Q9DDZ5
                     Q90WT9
Q9BEA8.
Q95M04
Q95N10
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Q9BDN1
Q9BDN1
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                                                                                                   Q96q17 homo sapien
Q971y0 mus musculu
Q9ese2 rattus norv
Q9jjk9 mus musculu
Q9jjk8 mus musculu
Q9jjk8 mus musculu
Q9jjk9 rattus norv
Q9ddz5 brachydanio
Q9ddz5 brachydanio
Q90wt9 gallus gall
Q9bea8 sus scrofa
Q95m04 sus scrofa
Q95m10 sus scrofa
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Q9bdm5
Q9bdn1
Q9bdn3
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                                 cercocebus callithrix
                                                                    macaca mula
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ID Q99
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Best Local Similarity ·
Matches 270; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q96Q17
Q96Q17;
Q1-DEC-2001
Q1-DEC-2001
Q1-DEC-2001
Q1-DEC-2001
HRANKL 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
IReda T., Kuroyama H., Hirokawa K.;
IReda T., Kuroyama H., Hirokawa K.;
"Human RANKL isoform.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB061227; BAB71768.1; -.
EMBL; AB061227; BAB71768.1; -.
SEQUENCE 270 AA; 30522 MW; 5C7754CE32E6F368 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
                             228
                                                                  121
                                                                                                       168
                                                                                                                                                                           108
                                                                                                                                        61
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SGDLATEYLQLMVYUTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGE
                                                      DTKLIPDSCRRIKQAFQGAVQKELQHIVGSQHTRAEKAMVDGSWLDLAKRSKLEAQPFAH 167
                                                                                                                                                                                                                        MFVALLGLGLGQVVCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQ 107
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                                                                                                                                                                                                                                                                                      Conservative
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(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 19, Last annotation updat
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                                                                                                                                                                                                                                                                                              84.48; Score 1422; DB 4; 1
100.08; Pred. No. 1.1e-121;
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Gene 230:121-127(1999).

EMBL; AB022039; BAA36970.1; JOINED EMBL; AB022036; BAA36970.1; JOINED EMBL; AB022038; BAA36970.1; JOINED EMBL; AB022038; BAA36970.1; JOINED HSSP; P50591; 1D0G.

MGD; MGD: 1100039; Tnfsfll.

InterPro; IPR0003263; TNF_5.

InterPro; IPR000478; TNF_family.

Pfam; PF00229; TNF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Last sequence up 01-DEC-2001 (TrEMBLrel. 19, Last annotation OSTECCLAST DIFFERENTIATION FACTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9R1Y0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ueda M., Higashio K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kodaira K., Kodaira
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=99214075;
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SMART; SM00207; TNF; 1.
PROSITE; PS50049; TNF_2; 1.
SEQUENCE 313 AA; 34719 MW;
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                                                                                                                                                                              VVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESEDT--LPDSCRRM
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                                                                                      KQAFQGAVQKELQHIVGPQRF---SAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGS
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DPDQDATYFGAFKVQDID 313
                                        DPDQDATYFGAFKVRDID 317
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ra K., Mizuno A., Yasuda
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Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83.6%; Score 1409; DB 11;
84.3%; Pred. No. 2.1e-120;
tive 16; Mismatches 28;
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Best Local
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01-OCT-2000 (TrEMBLrel. 15, L
01-DEC-2001 (TrEMBLrel. 19, L
RECEPTOR ACTIVATOR OF NF-KB L
TNFSF11 OR RANKL 2.
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Q9ESE2;
01-MAR-2001
01-MAR-2001
01-DEC-2001
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Bone Miner. Res. 15:2178-2186(2000).
EMBL; AF187319; AAG17031.1; -.
HSSP; P50591; 1DGG.
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01-MAR-2001 (TrEMBLrel. 16,
01-DEC-2001 (TrEMBLrel. 19,
RECEPTOR ACTIVATOR OF NE-KB
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                  Q9JJK9
Q9JJK9;
Q1-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR003263; TNF_5.
InterPro; IPR000478; TNF_family.
Pfam; PF00229; TNF; 1.
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PROSITE; PS50049; TNF_2
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                                   Eukaryota; Metazoa; Mammalia; Eutheria;
      NCBI_TaxID=10090
                                                                                                 Mus musculus
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262; Conserv
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ota; Metazoa; Chordata;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        318 AA;
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                                                                                                 (Mouse)
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Huang L., Gao X.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TNF_5; 1.
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                                   Chordata;
Rodentia;
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LIGAND.
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LIGAND 2.
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                                                                                                                                                                                                                                                            Created)
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Sciurognathi; Muridae; Murinae; Rattus
                                   Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
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Best Loc
Matches
                                                                                                                                                                                                                                                                                                                           Q9JJK8 PRELIMINARY; PRT; 199 AA.
Q9JJK8;
Q1-OCT-2000 (TrEMBLrel. 15, Created)
Q1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
RECEPTOR ACTIVATOR OF NF-KB LIGAND 3.
TNFSF11 OR RANKL 3.
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ProDom; PD008600; TNF_5; 1.
SMART; SM00207; TNF; 1.
PROSITE; PS50049; TNF_2; 1.
SEQUENCE 287 AA; 32234 MW;
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                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                Factor-kappaB Ligand Thymus.";
                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE-21150053; PubMed-11250921;
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InterPro; IPR003263; TNF_5.
InterPro; IPR003636; TNF_abc.
InterPro; IPR000478; TNF_family.
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SEQUENCE FROM N.A.
  Endocrinology 142:1419-1426(2001).
EMBL; AB032772; BAA97258.1; -.
                                                                           Ikeda T., Kasai M., Utsuyama M., Hirokawa K.;
"Determination of Three Isoforms of the Receptor Activator of Nuclear
Factor-kappaB Ligand and Their Differential Expression in Bone and
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P50591; 1D0G.
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hree Isoforms of the Receptor Activator of Nuclear
d and Their Differential Expression in Bone and
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Pred. No. 7.4e
16; Mismatches
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7.4e-108;
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RESULT Q9DDZ5 ID Q1 AC Q1

Q9DDZ5;

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Best Local
Matches 17
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InterPro; IPR003636; TNF_abc.
InterPro; IPR003636; TNF_family.
InterPro; IPR00478; TNF_family.
IPR00229; TNF; 1.
IPR00209; PNF_3; 1.
IPR0Dom; PD002012; TNF_abc; 1.
IPR0Dom; PD008600; TNF_5; 1.
IPR0STTPE; PS50049; TNF; 1.
IPROSTTPE; PS50049; PROSTTPE; PROSTTPE; PS50049; PROSTTPE; PROSTTPE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q91ZI9
Q91ZI9;
01-DEC-2001 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
TNFSF11 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                       Odgren P.R., Kim N., van Wesenbeeck L., MacKay C.A., Mas Safadi F.F., Popoff S.N., Lengner C., van Hul W., Chol Y "Evidence that the rat osteopetrotic mutation toothless the Tnfsf11 (TRANCE, RANKL, ODF, OPGL) gene."; Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AF425669; AAL23963.1; NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus
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MGD; MGI:1100089;
InterPro; IPR00326
                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-F344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10116;
119 IKQAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSG
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                                                                                                                                  1 Similarity 90.0
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oa; Chordata;
ia; Rodentia;
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90.6%;
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Last annotation update)
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Pred. No. 4.8e
11; Mismatches
                                                                                                                                  Score 262; DB 11;
Pred. No. 8.3e-17;
5; Mismatches 0;
                                                                                                                                                                                                                                                                                                           8A71E32F2B6A9410 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
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No. 4.8e-75;
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;

Cypriniformes; Cyprinidae; Danio.

NCBI_TaxID-7955;
                                                                                                                                                                                                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
TNF-RELATED APOPTOSIS INDUCING LIGAND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Molecular cloning and expression of a ligands in the fish ovary."; Comp. Biochem. Physiol. B, Comp. Bioche EMBL; AF250041; AAG47640.1; -.
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01-MAR-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
TRAIL-LIKE PROTEIN.
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases EMBL; AY057941; AAL23702.1; -. SEQUENCE 287 AA; 32092 MW; DB06E1C95087B108 CRC64;
                                                                             ovary."
                                                                                            SEQUENCE FROM N.A. Bridgham J.T., Johnson "TNF-related apoptosis
                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                             Q90WT9;
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ProDom; PD008600; TNF_5; 1.
SMART; SM00207; TNF; 1.
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InterPro; IPR000478; TNF_family.
Pfam; PF00229; TNF; 1.
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61; Conser
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Last sequence up
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Pred. No. 5.4e-14;
0; Mismatches 83;
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Best Local S
Matches 61
                                                 Query Match
Best Local
                                     Matches
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01-JUN-2001
01-JUN-2001
01-DEC-2001
                                                                                                                                                                                                                                           Tsuyuki S., Kono M., Bloom E.T.;
"Cloning and potential utility of porcine Fas
in porcine cells protects them from attack by
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ
EMBL; AB027297; BAB40919.1; -.
EMBL; AF397407; AAK84408.1; -.
                                                                                                PROSITE; PS00251; TNF_1; 1.
PROSITE; PS50049; TNF_2; 1.
SEQUENCE 282 AA; 31756 MW;
                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21322533; PubMed=11429161; Muneta Y., Shimoji Y., Inumaru S., Mo: "Molecular cloning, characterization, ligand (CD95 ligand).";
                                                                                                                                   PRINTS; PR01234; TNECROSISFCT PRODOM; PD002012; TNF_abc; 1. ProDom; PD008600; TNF_5; 1. SMART; SM00207; TNF; 1.
                                                                                                                                                                                            InterPro; IPR003263; TNF_5.
InterPro; IPR003636; TNF_abc.
InterPro; IPR000478; TNF_family.
                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FAS-LIGAND (FAS LIGAND).
Sus scrofa (Pig).
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22 PGAPHEGPLHAPPPPAPHQPPAA---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMVYVT-KTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VNEAQKSYFNISEGQVA--TKTLGKPSAHLIFRPQNPAQDGSSRRFGNLSQSCRHAITRW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        I-RAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIP-----SGSHKVSLSSW 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIKQAFQGAVQKELQHIVGSQH 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSEELRCLQLINQQQEGSNLEEL-----ISNQSCLKLANTIKAYVATVTENVISRSV 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EDSTIHSHLQNITYRDGRLRVNQAGKYYVYSQIYFRYSRDGAGARVSVPQLVQCINWKTS
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                                    76;
                                                  Similarity
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(TremBLrel. 17, Last seq
(TremBLrel. 19, Last ann
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                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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                                                  11.9%;
23.0%;
                                     42;
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Pred. No. 1.3e-11;
57; Mismatches 104
                                                  Score 200;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                  6743DAA1145671FB CRC64;
               SRSM--
                                       Mismatches
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                                                              Length
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                                     Indels 122;
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               -FVA
                                    Gaps
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112

95 52 37

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PGRP--GQRRPPPPPPPPPPPPTLLPSRPLPPLPPPSLKKKRDHNAGLCLLVMFFMVLVA

94

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STRAIN-BREED LANDRACE X LARGE YORKSHIRE WHITE (LW); TISSUE-LIVER; MOLEGI-TShiyama Y., Nakajima Y., Hoka S., Takagaki Y.; "Genomic Sequence Analysis of Pig Fas-Ligand Gene."; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AB069764; BAB64291.1; E54774EBF455127B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                          RSGEEISIEVSNPSLLDPDQDATYFGAFKV 313
                                                                                                                                                            INATDIPSGSHKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSG
          TSADHLYVNVSELSLVNFEESKTFFGLYKL
                                                                                               DLATEYLOLMVYVTKTSIKIPSSHTLMKGGSTKY-----WSGNSEFHFYSINVGGFFKL
                                                                                                                                PNSRSIP-----LEWEDTYGIALVSGVKYMKGSLVINDTGLYFVYSKVYFRGQYCN-
                                                                                                                                                                                                                            IPDSCRRIKQAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLT--
                                                                                                                                                                                                                                                                                    LLGLGLGQVVCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKL
                                                                                                                                                                                                                                                                                                                      PGRP---GQRRPPPPPPPPPPPTLLPSRPLPPLPPPSLKKKRDHNAGLCLLVMFFMVLVA 94
                                                                                                                                                                                                                                                               LVGLGLG-----MFQLFHLQKE----
                                                                                                                                                                                                                                                                                                                                                       PGAPHEGPLHAPPPPAPHQPPAA---SRSM-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TSADHLYVNVSELSLVNFEESKTFFGLYKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---NOPLSHKVY-TRNS-RYPODLVLMEGKMMNYCTTGOMWARSS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DLATEYLQLMVYVTKTSIKIPSSHTLMKGGSTKY-----WSGNSEFHFYSINVGGFFKL
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                                                                                                                                                                                              -----ESSLEKQIGHPNLPSEKK-------
                                                                  NQPLSHKVY-TRNS-RYPQDLVLMEGKMMNYCTTGQMWARSS-----YLGAVFNL
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l (TrEMBLrel. 19,
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Last sequence update)
Last annotation update)
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Pred. No. 3.9e-10;
                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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Sus.
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                                                        Q9MYL6 PRELIMINARY; PRT; 280 AA.

C Q9MYL6;
C Q9MYL6;
T Q1-OCT-2000 (TrEMBLrel. 15, Created)
T Q1-CT-2000 (TrEMBLrel. 15, Last sequence update)
T Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
E FAS LIGAND,
PT-FASL OR CM-FASL OR RM-FASL.
MACACA DEMESTRINA (Pig-tailed macaque),
S Macaca fascicularis (Crab eating macaque) (Cynomolgus macaca mulatta (Rhesus macaque).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
C Mammalia; Eutheria; Primates; Catarrhini; Cercopithecida;
NCBL_TaxID-9545, 9541, 9544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 75; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [1]
SEQUENCE FROM N.A.
Zhu N., Young Y.;
Zhu N., Young Y.;
"Molecular cloning and characterization of porcine Fas ligand
"Molecular cloning and characterization of porcine Fas ligand
Submitted (ARR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY033634; AAK56449.1; -.
EMBL; AY033634; AAK56449.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sus scrofa (Pig).
Eukaryota; Metazoa; Mammalia; Eutheria; MCBI_TaxID=9823;
SPECIES-M.nemestrina;
Kirii Y., Inoue T., Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q95N10;
Q95N10;
01-DEC-2001
01-DEC-2001
01-DEC-2001
                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LIGAND
                                                                                                                                                                                                                                                                                                                                                ADHLYVNVSELSLVNFEESKTFFGLYKL
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                                                                                                                                                                                                                                                                                                                                                                              GEEISIEVSNPSLLDPDQDATYFGAFKV
                                                                                                                                                                                                                                                                                                                                                                                                                                         ATEYLQLMVYVTKTSIKIPSSHTLMKGGSTKY-----WSGNSEFHFYSINVGGFFKLRS 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATDIPSGSHKVSLSSWYHDRGWAKISNWTFSNGKLIVNQDGFYYLYANIGFRHHETSGDL: | | ::| | |::|: | | ::|
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Yoshino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chordata; Craniata; Vertebrata; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11.8%;
22.9%;
             STRAIN-PIG-TAILED
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, Last sequence upo
, Last annotation :
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Pred. No. 4.9e
43; Mismatches
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               MONKEY;
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.9e-10;
                                                                                                                                     (Cynomolgus monkey), and
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                                                                                        Cercopithecidae;
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13;

FASL. FAS-LIGAND.

SEQUENCE FROM N.A. NCBI_TaxID=9823; Q95M04; Q95M04; Q1-DEC-2001 01-DEC-2001 01-DEC-2001

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253 284 205 230 154 170 125

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Best Local S
Matches 69
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InterPro; IPRO00478; TNF_family.
Pfam; PF00229; TNF; 1.
PFNITS; PR01234; TNECROSISFCT.
PRODOM; PD002012; TNF_abc; 1.
PRODOM; PD008600; TNF_5; 1.
SMART; SM00207; TNF; 1.
SMART; SM00207; TNF_1; 1.
PROSITE; PS00251; TNF_1; 1.
PROSITE; PS0049; TNF_2; 1.
SEQUENCE 280 AA; 31367 MW; F0B
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                                                         Q9BDM5;
01-JUN-2001 (TrEM
01-JUN-2001 (TrEM
01-DEC-2001 (TrEM
FAS ANTIGEN CD95.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPECIES-M.fascicularis; STRAIN-CYNOMOLGUS MONK Kirii Y., Inoue T., Yoshino K.; Kirii Y., Inoue T., Yoshino K.; Complete C "Cynomolgus monkey Fas ligand mRNA, complete C submitted (NOV-1999) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kirii Y., Inoue T., Yoshino K.;

"Rhesus monkey Fas ligand mRNA, complete cds."
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ
EMBL; AB035140; BAA90296.1; -
EMBL; AB035138; BAA90294.1; -
EMBL; AB035139; BAA90295.1; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR003263; TNF_5
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                     Macaca mulatta (Rhesus macaque).
Eukaryota; Metazoa; Chordata; Craniata;
Mammalia; Eutheria; Primates; Catarrhin
             Cercopithecinae;
                                                                                                                     Q9BDM5
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                                                                                                                                                                                                                                                                           ---LEWEDTYGIVLLSGVKYKKGGLVINETGLYFVYSKVYFR----
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                                                                                                                                                                                                                                                                                                                                                                                                                                   VTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLDP
                                                                                                                                                                                                                                                                                         VSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMVY
                                                                                                                                                                                                                                                                                                                                                                                                                      PPPPPPPPPPPPPPSPLPPLPPLKKRGNHSTGLCLLVMFFMVLVALVGLGLG-----
                                                                                                                                                                                EESQTFFGLYKL
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                                                                     1 (TrEMBLrel. 17, 11 (TrEMBLrel. 17, 11 (TrEMBLrel. 19, 11)
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                                                                                                                       PRELIMINARY;
               Macaca.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 186; DB 6;
Pred. No. 7.4e-09;
4; Mismatches 103
                                                                        Last sequence update)
Last annotation updat
                                                                                                Created)
                          Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F0B284D61A132EB4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                           --KELAELRESTSQKHTA------
                                                                                                                        280
                                      Vertebrata;
                           Cercopithecidae;
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J databases
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                                        Euteleostomi;
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RESULT
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Best Local
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InterPro; IPR003263; TWF_5.
InterPro; IPR003363; TWF_abc.
InterPro; IPR000478; TWF_abc.
InterPro; IPR000478; TWF_family.
InterPro; IPR000478; TWF_family.
Pfam; PF00229; TWF; 1.
PF10079; PR01234; TMFCROSISFCT.
PRODOM; PD002012; TWF_abc; 1.
PRODOM; PD00207; TWF_5; 1.
SMART; SM00207; TWF; 1.
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SEQUENCE FROM N.A.
VILLINGER F., BOSTIK P., Mayne A.E., King C...
Weiss W.R., Ansari A.A.;
"Cloning, sequencing, and homology analysis
"Cloning, and co-stimulatory molecules."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fas/Fas-ligand and co-stimulatory Immunogenetics 53:315-328(2001). EMBL, AF344856, AAK37539.1; -. HSSP; P01375; 4TSY.
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PROSITE; PS50049; TNF_2; 1.
SEQUENCE 280 AA; 31377 MW;
                                                                                                                                                                                              Q9BDN1;
                                                                                                                                            01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-DEC-2001 (TrEMBLrel. 19, CD95L PROTEIN.
SEQUENCE FROM N.A.
MEDLINE=21383618; PubMed=11491535;
Villinger F., Bostik P., Mayne A.E
Weiss W.R., Ansari A.A.;
                                                             Cercopithecinae;
NCBI_TaxID=9531;
                                                                           Cercocebus torquatus atys (Red-crowned mangabey) (Sooty mangabey). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Cercocebus.
                                                                                                                                 CD95L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          FQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLT--INATDIPSGSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---MFQLFHLQ----
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                                                                                                                                                                                                                                                                                                                                                    YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                    --SSLEKQIGH---
                                                                                                                                                                                                                                                                             FEESQTFFGLYKL
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                                                                                                                                                                                                                                                                                                    PDQDATYFGAFKV
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                                                                                                                                                                                                            PRELIMINARY;
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             Mayne A.E.,
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                                                                                                                                                           Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                PRT;
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                King C.L.,
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12;

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N [1]
P SEQUENCE FROM N.A.

A MEDILINE=21383618; PubMed=11491535;
A Willinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
A Weiss W.R., Ansari A.A.;
AR Weiss W.R., Ansari A.A.;

RT "Cloning, sequencing, and homology analysis of nonhuman prir
Fas/Fas-11gand and co-stimulatory molecules.";
RI Immunogenetics 53:315-328(2001).
DR EMBL, AF344844; AAK37603.1; -.
DR HSSP; P2995; 1ALY.
DR HSSP; P2995; 1ALY.
DR InterPro; IPR000478; TNF_family.
                                                             RESULT 15
Q9BN3
ID Q9BN3
AC Q9BN3
AC Q9BNN3
AC Q9BNN3
DT 01-JUN
DT 01-DC
CD154
OC CLLKary
OC ELKAry
OC ELKARY
OC ELKARY
RN (1)
RN SEQUEN
RX WEBLIN
RA Welss (1)
RP SEQUEN
RA Welss (1)
RT Fasfar
RL Immunos
DR ENBL;
DR HSSP;
DR Interp;
DR Interp;
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DR Interp;
DR Interp;
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Best Local Similarity
Matches 70; Conserv
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PRINTS; PRO1214; TNECROSISFCT.
PRODOM; PD002012; TNF_abc; 1.
PRODOM; PD008600; TNF_5; 1.
SMART; SM00207; TNF, 1.
PROSITE; PS00251; TNF_1; 1.
PROSITE; PS00251; TNF_1; 1.
PROSITE; PS00251; TNF_2; 1.
SEQUENCE 280 AA; 31407 MW; 7
                                                                                                                                                                                                                                                                                                                                                                                                          CD154 PROTEIN.

Callithrix jacchus (Common marmoset).

Cukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammaila; Eutheria; Primates; Platyrrhini; Callitrichidae; Callit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9BDN3;
                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9483;
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Immunogenetics 53:315-328(2001).

EMBL; AF344847; AAK37606.1; -.
HSSP; P01375; 478Y.

InterPro; IPR003295; P_rich_extensn.
InterPro; IPR003295; TNF_5.
InterPro; IPR003636; TNF_abc.
InterPro; IPR003636; TNF_abc.
InterPro; IPR003636; TNF_family.
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Pfam; PF00229; TNF; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --SSLEKQIGH-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLT--INATDIPSGSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIKQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PGAPHEGPLHAPPPPAPHQPP------AASRS------MFVALLGLGQVVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PPPPPPPPL--PPPPPPLPPLPLPPLKKRGNHSTGLCLLVMFFMVLVALVGLGLG----
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22.4%; Pred. No. 1.5e-08;
tive 44; Mismatches 100
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                                                                                                                                                                                                                                                                          Genain C.P.,
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Best Local Similarity 24.6
Matches 71; Conservative
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ProDom; PD008600; TNF_5; 1.
SMART; SM00207; TNF; 1.
PROSITE; PS00251; TNF_1; 1.
PROSITE; PS50049; TNF_2; 1.
SEQUENCE 261 AA; 29360 MW;
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                                                    TVKRQGLYYIYAQVTECSNREASSQAP-----FIASLCLKPPNRFERILLRAANTH--
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SSAKPCGQQSIHLGGIFELQPGASVFVNVTDPSQVSHGTGFTSFGLLKL
                       SGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLDPDQDATYFGAFKV
                                                                                IVNODGFYYLYANICFRHHETSGDLATEYLOLMVYVTKTSIKIPS--SHTLMKGGSTKYW
                                                                                                           SF-EMQKGDQ-NPQIAAHVISEAS-----SKTTSVLQW-AEKGYYTMSNNLVTLENGKQL
                                                                                                                                      SWLDLAKRSKLEAQPFAHLTINATDIPSGSHKVSLSSWYHDRGWAKISN--MTFSNGK-L
                                                                                                                                                                  NLHEDFVFMKTIQRCNTGERSLSLLNCEEIKSQFEGFV-KDIM-----LNKEEKKKEN 109
                                                                                                                                                                                   RLHENADFQDT--TLESQDTKLIPDSCRRIKQAFQGAVQKELQHIVGSQHIRAEKAMVDG
                                                                                                                                                                                                                          PVPRSAATGPPVSMKIFMYLLTVFLITQMIGSALFAVYLHRRLD--KIEDE-----R
                                                                                                                                                                                                                                                                                                 10.1%;
                                                                                                                                                                                                                                                                                  s; Score 169.5; DB 6;
s; Pred. No. 2.1e-07;
55; Mismatches 120;
                                                                                                                                                                                                                                                                                                                                                         10CA588D923754EB CRC64;
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